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rotein - protein search, using sw model

on: August 11, 2004, 13:00:42 ; Search time 45.7143 Seconds
(without alignments)
61.807 Million cell updates/sec

ect score: 47
ence: 1 GPCXXFXIRY 10

ing table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 1586107 seqs, 282547505 residues

l number of hits satisfying chosen parameters: 1586107

um DB seq length: 0
um DB seq length: 2000000000

rocessing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- base : A Geneseq 29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| lt | to | Score | Query Match | Length | DB ID | Description |
|----|----|-------|-------------|--------|----------|--------------------|
| 1 | 42 | 89.4 | 58 | 2 | AAR78567 | Aar78567 BPTI Kuni |
| 2 | 42 | 89.4 | 58 | 2 | AAR78568 | Aar78568 BPTI Kuni |
| 3 | 42 | 89.4 | 58 | 2 | AAR78569 | Aar78569 BPTI Kuni |
| 4 | 41 | 87.2 | 10 | 6 | ABU09383 | Abu09383 Consensus |
| 5 | 40 | 85.1 | 58 | 2 | AAR99175 | Aar99175 Genetical |
| 6 | 40 | 85.1 | 58 | 2 | AAR99176 | Aar99176 Genetical |
| 7 | 37 | 78.7 | 57 | 2 | AAR7436 | Aaw47436 Aprotinin |
| 8 | 37 | 78.7 | 57 | 2 | AAR7434 | Aaw47434 Aprotinin |
| 9 | 37 | 78.7 | 57 | 2 | AAR7432 | Aaw47432 Aprotinin |
| 10 | 37 | 78.7 | 57 | 2 | AAR7435 | Aaw47435 Aprotinin |
| 11 | 37 | 78.7 | 58 | 2 | AAR78552 | Aar78552 Human TFP |
| 12 | 37 | 78.7 | 58 | 2 | AAR99184 | Aar99184 Genetical |
| 13 | 37 | 78.7 | 60 | 2 | AAY08613 | Aay08613 Inter-alp |
| 14 | 37 | 78.7 | 128 | 2 | AAR82769 | Aaw82769 Bovine bi |
| 15 | 37 | 78.7 | 128 | 2 | AAR82766 | Aaw82766 Bovine bi |
| 16 | 37 | 78.7 | 128 | 2 | AAR82768 | Aaw82768 Bovine bi |
| 17 | 37 | 78.7 | 128 | 2 | AAR82764 | Aaw82764 Bovine bi |
| 18 | 37 | 78.7 | 128 | 2 | AAR82771 | Aaw82771 Bovine bi |
| 19 | 37 | 78.7 | 128 | 2 | AAR82767 | Aaw82767 Bovine bi |
| 20 | 37 | 78.7 | 128 | 2 | AAR82772 | Aaw82772 Bovine bi |
| 21 | 37 | 78.7 | 129 | 2 | AAR82765 | Aaw82765 Bovine bi |
| 22 | 36 | 76.6 | 25 | 1 | AAP91296 | Aap91296 Amino aci |
| 23 | 36 | 76.6 | 56 | 1 | AAP93399 | Aap93399 Aprotinin |
| 24 | 36 | 76.6 | 56 | 1 | AAP93398 | Aap93398 Aprotinin |
| 25 | 36 | 76.6 | 56 | 2 | AAR06714 | Aar06714 Synthetic |

ALIGNMENTS

RESULT 1

AAR78567 AAR78567 standard; peptide; 58 AA.

XX AAR78567;
XX AC
XX 01-MAR-1996 (first entry)
XX BPTI Kunitz domain derivative DPI-7.1.

XX Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.

XX Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 18
FT /note= "residue change: Ile to Phe"

XX W09518830-A2.

XX 13-JUL-1995.

XX 11-JAN-1995; 95WO-US000298.

XX 11-JAN-1994; 94US-00179658.

XX 10-MAR-1994; 94US-00208265.

XX (PROT-) PROTEIN ENG CORP.

XX Markland W, Ladner RC;

XX WPI; 1995-255042/33.

XX Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to prevent/treat disorders attributable to excess plasmin activity.

XX Example 2; Page 36; 59pp; English.

XX The peptides AAR78435-R78570 are derivatives of the Kunitz domains from a variety of plasmin inhibitors e.g. the human lipoprotein-associated coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were designed based on the Kunitz domains and are named designed plasmin inhibitor (DPI). This peptide is designed based on the bovine pancreatic trypsin inhibitor (BPTI) Kunitz domain (Kudom) (AAR78426). The peptides can be used to prevent or treat a clinical condition exacerbated by plasmin e.g. inappropriate fibrinolysis or fibrinogenolysis, excessive

CC bleeding associated with thrombolytics

XX Sequence 58 AA;

Query Match 89.4%; Score 42; DB 2; Length 58;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| ||||
Db 12 GPCRRFYRY 21

RESULT 2

AAR78568
ID AAR78568 standard; peptide; 58 AA.

XX AC AAR78568;

XX DT 01-MAR-1996 (first entry)

XX DE BPTI Kunitz domain derivative DPI-7.2.

XX Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 15 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

XX WO9518830-A2.

XX PN 13-JUL-1995.

XX PD 11-JAN-1995; 95WO-US000298.

XX PF 11-JAN-1994; 94US-00179658.

XX PR 10-MAR-1994; 94US-00208265.

XX PS (PROT-) PROTEIN ENG CORP.

XX PA Markland W, Ladner RC;

XX PI WPI; 1995-255042/33.

XX DR Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to

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XX PS Example 2; Page 36; 59pp; English.

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XX variety of plasmin inhibitors e.g. the human lipoprotein-associated

XX coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were

XX designed based on the Kunitz domains and are named Designed Plasmin

XX Inhibitor (DPI). This peptide is designed based on the bovine pancreatic

XX trypsin inhibitor (BPTI) Kunitz domain (KuDom) (AAR78426). The peptides

XX can be used to prevent or treat a clinical condition exacerbated by

XX plasmin e.g. inappropriate fibrinolysis or fibrinogenolysis, excessive

XX bleeding associated with thrombolytics

XX SQ Sequence 58 AA;

Query Match 89.4%; Score 42; DB 2; Length 58;

Best Local Similarity 70.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| ||||
Db 12 GPCRRFYRY 21

RESULT 4

ABU09383

ID ABU09383 standard; peptide; 10 AA.

XX AC ABU09383;

Db 12 GPCRRFYRY 21

RESULT 3

AAR78569

ID AAR78569 standard; peptide; 58 AA.

XX AC AAR78569;

XX DT 01-MAR-1996 (first entry)

XX DE BPTI Kunitz domain derivative DPI-7.3.

XX Human; lipoprotein-associated coagulation inhibitor; peptide library;

KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;

KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 15 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

FT FT Misc-difference 18 /note= "residue change: Lys to Arg"

XX WO9518830-A2.

XX PN 13-JUL-1995.

XX PD 11-JAN-1995; 95WO-US000298.

XX PF 11-JAN-1994; 94US-00179658.

XX PR 10-MAR-1994; 94US-00208265.

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XX PI WPI; 1995-255042/33.

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XX The peptides AAR78435-R78570 are derivatives of the Kunitz domains from a

XX variety of plasmin inhibitors e.g. the human lipoprotein-associated

XX coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were

XX designed based on the Kunitz domains and are named Designed Plasmin

XX Inhibitor (DPI). This peptide is designed based on the bovine pancreatic

XX trypsin inhibitor (BPTI) Kunitz domain (KuDom) (AAR78426). The peptides

XX can be used to prevent or treat a clinical condition exacerbated by

XX plasmin e.g. inappropriate fibrinolysis or fibrinogenolysis, excessive

XX bleeding associated with thrombolytics

XX SQ Sequence 58 AA;

Query Match 89.4%; Score 42; DB 2; Length 58;

Best Local Similarity 70.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| ||||
Db 12 GPCRRFYRY 21

RESULT 4

ABU09383

ID ABU09383 standard; peptide; 10 AA.

XX AC ABU09383;

17-JUL-2003 (first entry)

Consensus peptide sequence for mammalian Kunitz inhibitor.

Protein purification; protein isolation; recombinant fusion polypeptide; enzyme/tagged-peptide binding; fusion protein; tag peptide; recombinant capture protein; mammalian; Kunitz inhibitor.

Mammalia.

Synthetic.

Key Location/Qualifiers

Misc-difference 4

/label= Lys, Arg

Misc-difference 5

/label= Gly, Ala

Misc-difference 6

/label= Arg, Gly, Ser

EP1281716-A2.

05-FEB-2003.

06-JUL-2002; 2002EP-00015128.

10-JUL-2001; 2001US-00901996.

(HOFF) ROCHE DIAGNOSTICS GMBH.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Dwulet FE, Balgobin NG, McCarthy RC;

WPI; 2003-334999/32.

Purifying or isolating a recombinant fusion peptide, comprises forming a fusion peptide comprising a tag peptide covalently attached to a polypeptide and contacting the fusion peptide with an enzyme or modified enzyme.

Claim 9; Page 6; 17pp; English.

The present invention relates to a method for purifying or isolating a recombinant fusion polypeptide based on enzyme/tagged-peptide binding. The method comprises forming a fusion protein comprising a tag peptide sequence covalently attached to a polypeptide sequence, and contacting the fusion peptide with an enzyme or modified enzyme that specifically binds to the tag peptide sequence to form a complex between the enzyme or modified enzyme and the fusion peptide. The method of the invention is useful for purifying or isolating recombinant fusion polypeptides. The present method of using enzymes as capture agents offers several advantages not currently found in prior art. For example (a) it is possible to select natural or recombinant capture proteins with modified binding sites that will have different affinities for the same tag, (b) it is possible to modify the amino acid sequence of the tag to generate high, medium and low affinity peptide tags for use in different applications with the same capture protein, and (c) depending upon the application, natural or recombinant capture proteins with increased or decreased resistance to denaturation can also be prepared. Such versatility is amenable to the development of a variety of standardised binding and elution conditions for the isolation of tagged proteins or their complexes. ABU03283-ABU0395 represent peptides that may be used as tag peptides in the method of the present invention

Sequence 10 AA;

Query Match 87.2%; Score 41; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPCXXXFYRY 10

|||||

1 GPCXXXFYRY 10

RESULT 5

AAR99175
ID AAR99175 standard; protein; 58 AA.

XX
AC AAR99175;

XX
DT 12-FEB-1997 (first entry)

XX
DE Genetically engineered aprotinin-like Kunitz domain (DPI.2.2).

XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha1 antitrypsin; respiratory disorder; cystic fibrosis;
smokers emphysema.

XX
OS Synthetic.

XX
PN WO9620278-A2.

XX
PD 04-JUL-1996.

XX
PP 15-DEC-1995; 95WO-US016349.

XX
PR 16-DEC-1994; 94US-00358160.

XX
PA (PROT-) PROTEIN ENG CORP.

XX
PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX
DR WPI; 1996-321851/32.

XX
PT New engineered inhibitors of human neutrophil elastase - contg. aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or other respiratory disorders.

XX
PS Claim 1; Page 50; 105pp; English.

XX
CC Genetically engineered human derived Kunitz domains can be used to inhibit human neutrophil elastase, an enzyme involved in the elimination of pathogens and the restructuring of connective tissue. In cases of reduction of the circulating alpha-1-protease inhibitor (API or alpha1 antitrypsin), or the inactivation of API by oxidation (smokers emphysema), extensive destruction of the lung tissue may result from uncontrolled elastolytic activity of human neutrophil elastase. Other respiratory disorders such as cystic fibrosis are thought to be caused by human neutrophil elastase release by neutrophils. The genetically engineered human derived Kunitz domains can be used to treat such respiratory disorders. See AAR99146-R99211

XX
SQ Sequence 58 AA;

Query Match 85.1%; Score 40; DB 2; Length 58;

Best Local Similarity 60.0%; Pred. No. 2.7;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GPCXXXFYRY 10

|||||

Db 12 GPCIALFLRY 21

RESULT 6

AAR99176
ID AAR99176 standard; protein; 58 AA.

XX
AC AAR99176;

XX
DT 12-FEB-1997 (first entry)

XX
DE Genetically engineered aprotinin-like Kunitz domain (DPI.2.3).

XX
KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;

KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha 1 antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.
 XX Synthetic.
 XX WO9620278-A2.
 XX 04-JUL-1996.
 XX 15-DEC-1995; 95WO-US016349.
 XX 16-DEC-1994; 94US-00358160.
 XX (PROT-) PROTEIN ENG CORP.
 XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
 XX WPI; 1996-321851/32.
 XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
 PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.
 XX Claim 1; Page 50; 105pp; English.
 XX Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived Kunitz domains can be used to treat such
 CC respiratory disorders. See AAR99146-R99211
 XX
 SQ Sequence 58 AA;

Query Match 85.1%; Score 40; DB 2; Length 58;
 Best Local Similarity 60.0%; Pred. No. 2.7;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 ||| |||
 Db 12 GPCIAFLRY 21

RESULT 7
 AAW47436
 ID AAW47436 standard; peptide; 57 AA.

XX AAW47436;
 XX 26-JUN-1998 (first entry)
 XX Aprotinin variant 5.
 XX Aprotinin variant; serine protease inhibitor.

XX Homo sapiens.
 OS Synthetic.
 XX EP821007-A2.

XX 28-JAN-1998.
 XX 14-JUL-1997; 97EP-00111980.
 XX 25-JUL-1996; 96DE-01029982.
 XX (FARB) BAYER AG.

XX Schroeder W, Bjorn S, Norris K, Diness V, Norkekov-Lauritsen L;
 PI Christensen ND;
 XX WPI; 1998-102619/10.
 XX Aprotinin variants prepared by recombinant DNA techniques - useful as
 PT protease inhibitors in surgery and medicine.
 XX Claim 5; Fig 1; 19pp; German.
 XX The present sequence is an aprotinin variant, which can be used as a
 CC serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat
 CC multiple trauma, shock, pain, oedema, stroke and inflammation and to
 CC inhibit invasive tumour growth and metastasis, inflammation, coagulation
 CC and risk of haemorrhage in dialysis therapy and artificial organs.
 CC Compared with wild type aprotinin, the variant is less reactive with anti
 CC -aprotinin antibodies, less immunogenic, causes less histamine release
 CC from blood cells, exhibits reduced renal accumulation and has improved Ki
 CC values
 XX Sequence 57 AA;

Query Match 78.7%; Score 37; DB 2; Length 57;
 Best Local Similarity 60.0%; Pred. No. 9.8;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 ||| |||
 Db 11 GPCRSILRY 20

RESULT 8
 AAW47434
 ID AAW47434 standard; peptide; 57 AA.

XX AAW47434;
 XX 26-JUN-1998 (first entry)
 XX Aprotinin variant 3.
 XX Aprotinin variant; serine protease inhibitor.

XX Homo sapiens.
 OS Synthetic.
 XX EP821007-A2;

XX 28-JAN-1998.
 XX 14-JUL-1997; 97EP-00111980.
 XX 25-JUL-1996; 96DE-01029982.

XX (FARB) BAYER AG.

XX Schroeder W, Bjorn S, Norris K, Diness V, Norkekov-Lauritsen L;
 PI Christensen ND;
 XX WPI; 1998-102619/10.

XX Aprotinin variants prepared by recombinant DNA techniques - useful as
 PT protease inhibitors in surgery and medicine.

XX Claim 5; Fig 1; 19pp; German.

XX The present sequence is an aprotinin variant, which can be used as a
 CC serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat
 CC multiple trauma, shock, pain, oedema, stroke and inflammation and to
 CC inhibit invasive tumour growth and metastasis, inflammation, coagulation
 CC and risk of haemorrhage in dialysis therapy and artificial organs.
 CC Compared with wild type aprotinin, the variant is less reactive with anti

-aprotinin antibodies, less immunogenic, causes less histamine release from blood cells, exhibits reduced renal accumulation and has improved Ki values

Sequence 57 AA;

Query Match 78.7%; Score 37; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIIRY 10
||| |||
11 GPCRAAIIRY 20

JLT 9
17432

AAW47432 standard; peptide; 57 AA.

AAW47432;

26-JUN-1998 (first entry)

Aprotinin variant 1.

Aprotinin variant; serine protease inhibitor.

Homo sapiens.
Synthetic.

EP821007-A2.

28-JAN-1998.

14-JUL-1997; 97EP-00111980.

25-JUL-1996; 96DE-01029982.

(FARB) BAYER AG.

Schroeder W, Bjorn S, Norris K, Diness V, Norkkov-Lauritsen L;
Christensen ND;

WPI; 1998-102619/10.

Aprotinin variants prepared by recombinant DNA techniques - useful as
protease inhibitors in surgery and medicine.

Claim 5; Page 13; 19pp; German.

The present sequence is an aprotinin variant, which can be used as a
serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat
multiple trauma, shock, pain, oedema, stroke and inflammation and to
inhibit invasive tumour growth and metastasis, inflammation, coagulation
and risk of haemorrhage in dialysis therapy and artificial organs.
Compared with wild type aprotinin, the variant is less reactive with anti
-aprotinin antibodies, less immunogenic, causes less histamine release
from blood cells, exhibits reduced renal accumulation and has improved Ki
values

Sequence 57 AA;

Query Match 78.7%; Score 37; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIIRY 10
||| |||
11 GPCRAAIIRY 20

JLT 10
7435

ID AAW47435 standard; peptide; 57 AA.
XX AAW47435;
XX
DT 26-JUN-1998 (first entry)
XX
DE Aprotinin variant 4.
XX
KW Aprotinin variant; serine protease inhibitor.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP821007-A2.
XX
PD 28-JAN-1998.
XX
PF 14-JUL-1997; 97EP-00111980.
XX
PR 25-JUL-1996; 96DE-01029982.
XX
PA (FARB) BAYER AG.
XX
PI Schroeder W, Bjorn S, Norris K, Diness V, Norkkov-Lauritsen L;
PI Christensen ND;
XX
DR WPI; 1998-102619/10.
XX
XX
PT Aprotinin variants prepared by recombinant DNA techniques - useful as
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XX
PS Claim 5; Fig 1; 19pp; German.
XX
CC The present sequence is an aprotinin variant, which can be used as a
CC serine protease inhibitor, e.g. in surgery to reduce blood loss, to treat
CC multiple trauma, shock, pain, oedema, stroke and inflammation and to
CC inhibit invasive tumour growth and metastasis, inflammation, coagulation
CC and risk of haemorrhage in dialysis therapy and artificial organs.
CC Compared with wild type aprotinin, the variant is less reactive with anti
CC -aprotinin antibodies, less immunogenic, causes less histamine release
CC from blood cells, exhibits reduced renal accumulation and has improved Ki
CC values
XX
SQ Sequence 57 AA;
XX
Query Match 78.7%; Score 37; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GPCXXXFIIRY 10
||| |||
Db 11 GPCRAAIIRY 20
RESULT 11
AAR78552
ID AAR78552 standard; peptide; 58 AA.
XX
AC AAR78552;
XX
DT 01-MAR-1996 (first entry)
XX
DE Human TPPI-2 domain 3 KuDOM derivative DPI-3.3.1.
XX
KW Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 11 /note="residue change: Glu to Thr"
FT

FT Misc-difference 13 /note= "residue change: Leu to Pro"
 FT Misc-difference 15 /note= "residue change: Ser to Arg"
 FT Misc-difference 17 /note= "residue change: Asn to Arg"
 FT Misc-difference 18 /note= "residue change: Val to Phe"
 FT Misc-difference 36 /note= "residue change: Thr to Gly"
 XX W09518830-A2.
 XX 13-JUL-1995.
 XX 11-JAN-1995; 95WO-US000298.
 XX 11-JAN-1994; 94US-00179658.
 XX 10-MAR-1994; 94US-00208265.
 XX (PROT-) PROTEIN ENG CORP.
 XX Markland W, Ladner RC;
 XX WPI; 1995-255042/33.
 XX Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to
 XX prevent/treat disorders attributable to excess plasmin activity.
 XX Claim 3; Page 34; 59pp; English.
 XX The peptides AAR78435-R78570 are derivatives of the Kunitz domains from a
 XX variety of plasmin inhibitors e.g. the human lipoprotein-associated
 XX coagulation inhibitor (LACI) Kunitz domains 1, 2 or 3. The peptides were
 XX designed based on the Kunitz domains and are named Designed Plasmin
 XX Inhibitor (DPI). This peptide is designed based on the human TPPI-2
 XX domain 3 Kunitz domain (KUDom) (AAR78551). The peptides can be used to
 XX prevent or treat a clinical condition exacerbated by plasmin e.g.
 XX inappropriate fibrinolysis or fibrinogenolysis, excessive bleeding
 XX associated with thrombolytics
 XX Sequence 58 AA;
 XX Query Match 78.7%; Score 37; DB 2; Length 58;
 XX Best Local Similarity 60.0%; Pred. No. 9.9;
 XX Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GPCXXXFYRY 10
 DB 12 GPCARFTRY 21
 RESULT 12
 AAR99184
 ID AAR99184 standard; protein; 58 AA.
 XX AAR99184;
 XX 12-FEB-1997 (first entry)
 XX Genetically engineered aprotinin-like Kunitz domain (DPI.4.3).
 XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 XX alaph antitrypsin; respiratory disorder; cystic fibrosis;
 XX smokers emphysema.
 XX Synthetic.
 XX W09620278-A2.
 XX 04-JUL-1996.
 XX Transgenic mice useful for studying compounds potentially useful in the

PP 15-DEC-1995; 95WO-US016349.
 XX 16-DEC-1994; 94US-00358160.
 XX (PROT-) PROTEIN ENG CORP.
 XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
 XX WPI; 1996-321851/32.
 XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
 XX -like Kunitz domain for treating, e.g. cystic fibrosis or other
 XX respiratory disorders.
 XX Claim 1; Page 51; 105pp; English.
 XX Genetically engineered human derived Kunitz domains can be used to
 XX inhibit human neutrophil elastase, an enzyme involved in the elimination
 XX of pathogens and the restructuring of connective tissue. In cases of
 XX reduction of the circulating alpha-1-protease inhibitor (API or alpha1
 XX antitrypsin), or the inactivation of API by oxidation (smokers
 XX emphysema), extensive destruction of the lung tissue may result from
 XX uncontrolled elastolytic activity of human neutrophil elastase. Other
 XX respiratory disorders such as cystic fibrosis are thought to be caused by
 XX human neutrophil elastase release by neutrophils. The genetically
 XX engineered human derived Kunitz domains can be used to treat such
 XX respiratory disorders. See AAR99146-R99211
 XX Sequence 58 AA;
 XX Query Match 78.7%; Score 37; DB 2; Length 58;
 XX Best Local Similarity 60.0%; Pred. No. 9.9;
 XX Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GPCXXXFYRY 10
 DB 12 GPCIAFFTRY 21
 RESULT 13
 AAY08613
 ID AAY08613 standard; protein; 60 AA.
 XX AAY08613;
 XX 05-AUG-1999 (first entry)
 XX Inter-alpha-trypsin inhibitor (BPI type) protein fragment TIBOR.
 XX APP; beta-amyloid precursor protein; human; transgenic mice; pathology;
 XX Alzheimer's disease; model; therapeutic compound; brain; mechanism;
 XX nerve tissue specific promoter; synthesis; inhibitor; deposition;
 XX plaque formation; treatment.
 XX Unidentified.
 XX US5912410-A.
 XX 15-JUN-1999.
 XX 13-APR-1995; 95US-00422333.
 XX 15-JUN-1990; 90US-00538857.
 XX 17-JUN-1991; 91US-00716725.
 XX 21-OCT-1994; 94US-00327381.
 XX (SCIO-) SCIOS INC.
 XX Cordell B;
 XX WPI; 1999-357231/30.
 XX Transgenic mice useful for studying compounds potentially useful in the

treatment of Alzheimer's disease.

Disclosure; Fig 8B; 72pp; English.

This invention describes novel transgenic mice expressing proteins related to the pathology of Alzheimer's disease and which provide models for studying potentially therapeutic compounds. The transgenic mice contain a DNA sequence encoding a beta-amyloid precursor protein (APP) and a nerve tissue specific promoter operably linked to the beta-APP allowing its expression to form beta-amyloid protein deposits in the animal's brain. The transgenic mouse is useful for elucidating the molecular mechanisms involved in the synthesis of and, more importantly, inhibiting the synthesis and deposition of beta-amyloid proteins (most importantly in the brain where plaque formation is associated with Alzheimer's disease) by inhibiting production and/or increasing cleavage after production. The transgenic animals provide useful models for studying the in vivo relationships of the proteins to each other and to other compounds being tested for their usefulness in treating Alzheimer's disease

Sequence 60 AA;

Query Match 78.7%; Score 37; DB 2; Length 60;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFIRY 10
|||
14 GPCXAMIRY 23

LT 14

2769

AAW82769 standard; peptide; 128 AA.

AAW82769;

22-APR-1999 (first entry)

Bovine bikunin peptide variant #6.

Aprotinin; bovine; pancreatic trypsin inhibitor; BPTI; variant; bikinin; inhibitor; kallikrein; plasmin; factor Xa; elastase; blood loss; shock; thromboembolic disorder; polytrauma; sepsis; coagulation; organ failure; angina; myocardial infarct; stroke; embolism; thrombosis; restenosis; perfusion injury; inflammatory disorder; tumour invasion; metastasis; pain; oedema; haemostasis; dialysis.

Bos taurus.
Synthetic.

DE19725014-A1.

17-DEC-1998.

13-JUN-1997; 97DE-01025014.

13-JUN-1997; 97DE-01025014.

(FARB) BAYER AG.

Schroeder W, Apeler H;

WPI; 1999-046858/05.

Ne aprotinin and bikunin variants - useful for reducing blood loss during surgery, for treating e.g. thromboembolic disorders.

Disclosure; Fig 2; 40pp; German.

AAW82763-W82772 represent variants of the bovine bikunin peptide which is composed of two aprotinin (also known as bovine pancreatic trypsin inhibitor, BPTI) that have a net charge of +3 to -3 at pH 7. The

CC aprotinins are kallikrein, plasmin and factor Xa inhibitors. The bikunins
CC are kallikrein, plasmin, factor Xa and elastase inhibitors. The
CC aprotinins and bikunins can be used to reduce blood loss during surgery,
CC to treat thromboembolic disorders, shock, polytrauma, sepsis,
CC disseminated intravascular coagulation, multi-organ failure, unstable
CC angina, myocardial infarct, stroke, embolism, deep vein thrombosis,
CC restenosis, perfusion injury, thrombosis and bleeding after thrombosis,
CC to treat inflammatory disorders, to inhibit tumour invasion and
CC metastasis, to treat pain and oedema and to inhibit haemostasis
CC activation during dialysis. The variants have altered or enhanced
CC protease inhibition specificities

XX Sequence 128 AA;

SQ

Query Match 78.7%; Score 37; DB 2; Length 128;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFIRY 10

|||

DB 82 GPCRAAIRY 91

RESULT 15

AAW82766

ID AAW82766 standard; peptide; 128 AA.

XX

AC AAW82766;

XX 22-APR-1999 (first entry)

XX Bovine bikunin peptide variant #3.

DE Aprotinin; bovine; pancreatic trypsin inhibitor; BPTI; variant; bikinin;
KW inhibitor; kallikrein; plasmin; factor Xa; elastase; blood loss; shock;
KW thromboembolic disorder; polytrauma; sepsis; coagulation; organ failure;
KW angina; myocardial infarct; stroke; embolism; thrombosis; restenosis;
KW perfusion injury; inflammatory disorder; tumour invasion; metastasis;
KW pain; oedema; haemostasis; dialysis.

XX Bos taurus.

OS Synthetic.

XX DE19725014-A1.

PN 17-DEC-1998.

XX 13-JUN-1997; 97DE-01025014.

XX 13-JUN-1997; 97DE-01025014.

XX (FARB) BAYER AG.

XX Schroeder W, Apeler H;

XX WPI; 1999-046858/05.

XX Ne aprotinin and bikunin variants - useful for reducing blood loss during surgery, for treating e.g. thromboembolic disorders.

XX Disclosure; Fig 2; 40pp; German.

XX AAW82764-W82772 represent variants of the bovine bikunin peptide which is
CC composed of two aprotinin (also known as bovine pancreatic trypsin
CC inhibitor, BPTI) that have a net charge of +3 to -3 at pH 7. The
CC aprotinins are kallikrein, plasmin and factor Xa inhibitors. The bikunins
CC are kallikrein, plasmin, factor Xa and elastase inhibitors. The
CC aprotinins and bikunins can be used to reduce blood loss during surgery,
CC to treat thromboembolic disorders, shock, polytrauma, sepsis,
CC disseminated intravascular coagulation, multi-organ failure, unstable
CC angina, myocardial infarct, stroke, embolism, deep vein thrombosis,
CC restenosis, perfusion injury, thrombosis and bleeding after thrombosis,
CC to treat inflammatory disorders, to inhibit tumour invasion and

CC metastasis, to treat pain and oedema and to inhibit haemostasis
CC activation during dialysis. The variants have altered or enhanced
CC protease inhibition specificities
XX

SQ Sequence 128 AA;

Query Match 78.7%; Score 37; DB 2; Length 128;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GPCXXXPTRY 10

|||

Db 82 GPCRAAIY 91

Search completed: August 11, 2004, 13:07:39

Job time : 46.7143 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: August 11, 2004, 13:04:58 ; Search time 10.9524 Seconds
(without alignments)
87.827 Million cell updates/sec

ect score: 47

ence: 1 GPCXXXFIRY 10

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283366 seqs, 96191526 residues

l number of hits satisfying chosen parameters: 283366

um DB seq length: 0

um DB seq length: 2000000000

-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ibase : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| lt | Score | Query Match | Length | ID | Description |
|----|-------|-------------|--------|----------|-----------------------------------|
| 1 | 42 | 89.4 | 122 | 1 A55115 | uterine plasmin/trypsin inhibitor |
| 2 | 39 | 83.0 | 57 | 2 A59204 | basic proteinase i |
| 3 | 37 | 78.7 | 60 | 1 TIBOR | serum basic protei |
| 4 | 36 | 76.6 | 58 | 2 S10063 | isoaprotinin G2 - |
| 5 | 36 | 76.6 | 59 | 2 S00371 | isoaprotinin G1 - |
| 6 | 36 | 76.6 | 100 | 1 TIBO | basic proteinase i |
| 7 | 36 | 76.6 | 100 | 1 TIBOSP | spleen basic prote |
| 8 | 35 | 74.5 | 61 | 1 TIHCEP | proteinase inhibit |
| 9 | 35 | 74.5 | 62 | 2 S07451 | proteinase inhibit |
| 10 | 35 | 74.5 | 67 | 1 TIBOC | trypsin inhibitor, |
| 11 | 35 | 74.5 | 324 | 2 AB0767 | trypsin inhibitor, |
| 12 | 35 | 74.5 | 330 | 1 S15303 | probable CDP-6-deo |
| 13 | 35 | 74.5 | 580 | 2 T20716 | hypothetical prote |
| 14 | 35 | 74.5 | 2225 | 2 T26063 | hypothetical prote |
| 15 | 34 | 72.3 | 51 | 2 I68704 | MHC c5/gli. protein |
| 16 | 34 | 72.3 | 123 | 2 A29652 | inter-alpha-trypsi |
| 17 | 34 | 72.3 | 235 | 2 A54951 | tissue factor path |
| 18 | 34 | 72.3 | 250 | 2 I48850 | TL antigen - mouse |
| 19 | 34 | 72.3 | 352 | 1 TI00BI | alpha-1-microglobu |
| 20 | 34 | 72.3 | 361 | 2 B25132 | MHC class I histoc |
| 21 | 34 | 72.3 | 361 | 2 I48851 | TL antigen - mouse |
| 22 | 34 | 72.3 | 372 | 2 A25148 | thymus leukemia an |
| 23 | 34 | 72.3 | 384 | 2 A25132 | MHC class I histoc |
| 24 | 34 | 72.3 | 384 | 2 I54499 | MHC thymus leukemi |
| 25 | 33 | 70.2 | 30 | 2 S07484 | proteinase inhibit |
| 26 | 33 | 70.2 | 53 | 2 B29235 | hemolymph trypsin |
| 27 | 33 | 70.2 | 1553 | 2 T09361 | hypothetical prote |
| 28 | 32 | 68.1 | 56 | 2 JN0380 | trypsin inhibitor |
| 29 | 32 | 68.1 | 58 | 1 TIHABK | isoinhibitor K (BP |

TL antigen - mouse
alkaline exonuclea
hepatocyte growth
serine-repeat anti
aspartate transami
hypothetical prote
hypothetical prote
serine-repeat anti
SERA antigen/papai
genome polyprotein
hypothetical prote
alanine-trna ligas
C. perfringens tra
hypothetical prote
S'-amp-activated p
SIP2 protein homol
hypothetical prote

ALIGNMENTS

RESULT 1

A55115
uterine plasmin/trypsin inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55115
R;Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
J. Biol. Chem. 269, 24090-24094, 1994
A;Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase inh
A;Reference number: A55115; MUID:95014140; PMID:7929061
A;Accession: A55115
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <STA>
A;Cross-references: GB:L14282; NID:9682652; PIDN:AAAG2425.1; PID:G682653
A;Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolo
C;Keywords: serine proteinase inhibitor
F;38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match

89.4%; Score 42; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 0.071;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPCXXXFIRY 10

Db 45 GPCSAHFVRY 54

RESULT 2

A59204
basic proteinase inhibitor - great pond snail
N;Alternate names: trypsin inhibitor
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 17-Mar-2000
C;Accession: A59204
R;Nagle, G.
submitted to the Protein Sequence Database, March 2000
A;Description: Lymnaea trypsin inhibitor.
A;Reference number: A59204
A;Accession: A59204
A;Molecule type: protein
A;Residues: 1-57 <NAG>
A;Experimental source: albumen gland
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolo
F;5-55/Domain: animal Kunitz-type proteinase inhibitor
F;5-55,14-38,30-51/Disulfide bonds: #status predicted
F;15/inhibitory site: Lys (trypsin) #status predicted
F;24/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

83.0%; Score 39; DB 2; Length 57;

Best Local Similarity 60.0%; Pred. No. 0.16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| |||
Db 12 GPCXGNFLRY 21

RESULT 3

TIBOR
serum basic proteinase inhibitor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Oct-1990 #sequence_revision 31-Oct-1980 #text_change 31-Dec-1993
C;Accession: A01206
R;Wachter, E.; Deppner, K.; Hochstrasser, K.; Lempart, K.; Geiger, R.
FEBS Lett. 119, 58-62, 1980
A;Title: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination
A;Reference number: A01206; MUID:81044408; PMID:7428928
A;Accession: A01206
A;Molecule type: protein
A;Residues: 1-60 <WAC>
C;Comment: This inhibitor has activity very similar to that of the basic proteinase inhibitor
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F;17/Inhibitory site: Lys (trypsin) #status experimental

Query Match 78.7%; Score 37; DB 1; Length 60;
Best Local Similarity 60.0%; Pred. No. 0.46;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| |||
Db 14 GPCXAMRY 23

RESULT 4

isoaprotinin G2 - bovine hybrid
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Jun-1997
C;Accession: S10063
R;Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bovine
A;Reference number: S00371; MUID:88221840; PMID:2453200
A;Accession: S10063
A;Molecule type: protein
A;Residues: 1-58 <SIE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F;15/Inhibitory site: Lys (trypsin) #status predicted

Query Match 76.6%; Score 36; DB 2; Length 58;
Best Local Similarity 60.0%; Pred. No. 0.73;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| |||
Db 12 GPCXAMRY 21

RESULT 5

isoaprotinin G1 - bovine hybrid
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Jun-1997
C;Accession: S00371
R;Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bovine
A;Reference number: S00371; MUID:88221840; PMID:2453200

A;Accession: S00371
A;Molecule type: protein
A;Residues: 1-59 <SIE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;6-56/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 76.6%; Score 36; DB 2; Length 59;
Best Local Similarity 60.0%; Pred. No. 0.74;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
||| |||
Db 13 GPCXAMRY 22

RESULT 6

TIBO
basic proteinase inhibitor precursor - bovine
N;Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikrein; Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 22-Jul-1994 #text_change 16-Jun-2000
C;Accession: S00277; A30333; S10546; S02486; S28197; A90162; A92023; A90927; J. Mol. Biol. 194, 11-22, 1987
R;Creighton, T.E.; Charles, I.G.
A;Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibitors
A;Reference number: S00274; MUID:87283304; PMID:2441071
A;Accession: S00277
A;Molecule type: DNA; mRNA
A;Residues: 1-100 <CR2>
A;Cross-references: GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1; PID:g162769
R;Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A;Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor
A;Reference number: A90926; MUID:88295740; PMID:2456884
A;Accession: A30333
A;Molecule type: DNA
A;Residues: 1-100 <CRE>
A;Cross-references: GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1; PID:g162769
R;Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A;Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic
A;Reference number: S10546; MUID:86158754; PMID:2420326
A;Accession: S10546
A;Molecule type: DNA
A;Residues: 34-97 <KIN>
R;Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
A;Title: Aprotinin-like inhibitors in bovine organs.
A;Reference number: S02485; MUID:89076531; PMID:2462435
A;Accession: S02486
A;Molecule type: protein
A;Residues: 36-93 <FIO>
R;Ikemita, M.; Jone, C.S.; Kamo, M.; Tsugita, A.; Kizuka, K.; Moriya, H.
Protein Seq. Data Anal. 5, 7-11, 1992
A;Title: Purification and characterization of the major cationic kallikrein inhibitor
A;Reference number: S28197; MUID:93150003; PMID:1283464
A;Accession: S28197
A;Molecule type: protein
A;Residues: 36-93 <IKK>
R;Kassell, B.; Lastowski, M.
Biochem. Biophys. Res. Commun. 20, 463-468, 1965
A;Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
A;Reference number: A90162; MUID:66083012; PMID:5860161
A;Contents: annotation; disulfide bonds
A;Accession: A90162
A;Molecule type: protein
A;Residues: 36-93 <KAS>
R;Anderer, F.A.; Hornle, S.
J. Biol. Chem. 241, 1568-1572, 1966
A;Title: The disulfide linkages in kallikrein inactivator of bovine lung.

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains.

F;34-98/Product: spleen inhibitor I #status experimental <SI1>
 F;36-97/Product: spleen inhibitor III #status experimental <SI3>
 F;36-93/Product: spleen inhibitor II #status experimental <SI2>
 F;40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F;40-90,49-73,65-86/Disulfide bonds: #status predicted
 F;50/Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein) #status predicted

Query Match 76.6%; Score 36; DB 1; Length 100;
 Best Local Similarity 60.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 |||||

DB 47 GPCAKMIRY 56
 |||||

RESULT 8

TIRCP

Proteinase inhibitor (BPI-type) - horseshoe crab (Tachyplesus tridentatus)

C;Species: Tachyplesus tridentatus

C;Date: 08-Mar-1989 #sequence_revision 22-Jul-1994 #text_change 24-Feb-1995

C;Accession: A26923

R;Nakamura, T.; Hirai, T.; Tokunaga, F.; Kawabata, S.; Iwanaga, S.

J. Biochem. 101, 1297-1306, 1987

A;Title: Purification and amino acid sequence of Kunitz-type protease inhibitor found in

A;Reference number: A26923; PMID:3308864

A;Accession: A26923

A;Molecule type: protein

A;Residues: 1-61 <NAK>

A;Experimental source: hemocytes

A;Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;8-58,17-41,33-54/Disulfide bonds: #status predicted

F;18/Inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)

Query Match 74.5%; Score 35; DB 1; Length 61;

Best Local Similarity 60.0%; Pred. No. 1.3;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 |||||

DB 15 GPCRAGPKRY 24
 |||||

RESULT 9

S07451

Proteinase inhibitor 5.II - snake-locks sea anemone

C;Species: Anemonia sulcata (snake-locks sea anemone)

C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997

C;Accession: S07451; B27222

R;Wunderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1991

A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia s

A;Reference number: S07451

A;Accession: S07451

A;Molecule type: protein

A;Residues: 1-59 <WUN>

A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R;Krebs, H.C.; Habermehl, G.G.

Naturwissenschaften 74, 395-396, 1987

A;Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der s

A;Reference number: A94700

A;Accession: B27222

A;Molecule type: protein

A;Residues: 1-38, 'R', 40, 'B', 42, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRE>

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: serine proteinase inhibitor

F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 74.5%; Score 35; DB 2; Length 62;

Best Local Similarity 60.0%; Pred. No. 1.3;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 |||||

DB 12 GPCRAFPRY 21
 |||||

RESULT 10

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 06-Dec-1996

C;Accession: A01207

R;Cechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun. 36, 3342-3357, 1971

A;Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A;Reference number: A90928

A;Accession: A01207

A;Molecule type: protein

A;Residues: 1-26, 'B', 28-67 <CEC>

A;Note: the residue identified as Asx is bound to carbohydrate; therefore, we have shc

R;Cechova, D.; Ber, E.

Collect. Czech. Chem. Commun. 39, 680-688, 1974

A;Title: Disulfide bonds of trypsin inhibitor from cow colostrum.

A;Reference number: A90929

A;Contents: annotation; disulfide bonds

R;Cechova, D.; Muszynska, G.

FEBS Lett. 8, 84-86, 1970

A;Title: Role of lysine 18 in active center of cow colostrum trypsin inhibitor.

A;Reference number: A91440

A;Contents: annotation

A;Note: the inhibitory site was determined

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor

C;Keywords: colostrum; glycoprotein; serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;8-58,17-41,33-54/Disulfide bonds: #status experimental

F;18/Inhibitory site: Lys (trypsin) #status experimental

F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 74.5%; Score 35; DB 1; Length 67;

Best Local Similarity 50.0%; Pred. No. 1.4;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
 |||||

DB 15 GPCKAALLRY 24
 |||||

RESULT 11

AB0767

Probable reductase RfBI rfbI [imported] - Salmonella enterica subsp. enterica serovar

C;Species: Salmonella enterica subsp. enterica serovar typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AB0767

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churchc

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, I

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se;

A;Reference number: AB0502; PMID:11677608

A;Accession: AB0767

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-324 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD02456.1; PID:gi16503323; GSPDB:GN00176

C;Genetics:

A;Gene: rfbI

C;Superfamily: methanone monooxygenase reductase component; cytochrome-b5 reductase hom

Query Match 74.5%; Score 35; DB 2; Length 324;

Best Local Similarity 66.7%; Pred. No. 5.4;

atches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 GPCXXXFIR 9
184 GPCGTFIR 192

LT 12
03
able CDP-6-deoxy-Delta(3,4)-glucoseen reductase (EC 1.3.1.1) - Salmonella typhimurium
ternate names: hypothetical protein 7.6
ecies: Salmonella typhimurium
te: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
ession: S15303
aug, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
Microbiol. 5, 695-713, 1991
le: Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar
ference number: S15296; MUID:91260454; PMID:1710759
ession: S15303
atus: preliminary
lecle type: DNA
sidues: 1-330 <MOL>
perfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolo
ywords: 2Fe-2S; iron-sulfur protein; metalloprotein; oxidoreductase
-72/Domain: ferredoxin [2Fe-2S] homology <FER>
l-320/Domain: cytochrome-b5 reductase homology <CBR>
,42,45,71/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
ery Match 74.5%; Score 35; DB 1; Length 330;
st Local Similarity 66.7%; Pred. No. 5.4;
atches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GPCXXXFIR 9
184 GPCGTFIR 192

LT 13
16
thetical protein F10F2.8 - Caenorhabditis elegans
ecies: Caenorhabditis elegans
te: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
ession: T20716
les, L.
itted to the EMBL Data Library, August 1994
ference number: Z19313
ession: T20716
atus: preliminary; translated from GB/EMBL/DBJ
lecle type: DNA
sidues: 1-580 <MIL>
ross-references: EMBL:Z35598; PIDN:CAA84654.1; GSPDB:GN00021; CESP:F10F2.8
perimental source: clone F10F2
netics:
ne: CESP:F10F2.8
up position: 3
trons: 46/3; 64/3; 151/1; 330/3; 365/2; 453/1
ery Match 74.5%; Score 35; DB 2; Length 580;
st Local Similarity 50.0%; Pred. No. 8.9;
atches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 GPCXXXFIR 10
395 GPCPAGEFLO 404

LT 14
63
thetical protein W01F3.3 - Caenorhabditis elegans
ecies: Caenorhabditis elegans
te: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
ession: T26063
ummings, P.

submitted to the EMBL Data Library, March 1997
A;Reference number: Z20145
A;Accession: T26063
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
A;Experimental source: clone W01F3
C;Genetics:
A;Gene: CESP:W01F3.3
A;Map position: 5
A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
Query Match 74.5%; Score 35; DB 2; Length 2225;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPCXXXFIR 10
DB 470 GPCGSPQRY 479

RESULT 15
I68704
MHC c5/gII protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I68704
R;Rogers, J.H.
Immunogenetics 21, 343-353, 1985
A;Title: Family organization of mouse H-2 class I genes.
A;Reference number: I54413; MUID:85206117; PMID:3997208
A;Accession: I68704
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-91 <RES>
A;Cross-references: GB:M14828; NID:G199643; PIDN:AAA39688.1; PID:G554240
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 72.3%; Score 34; DB 2; Length 91;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPCXXXFIR 10
DB 71 GPCGSLRY 80

Search completed: August 11, 2004, 13:09:58
Job time : 10.9524 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: August 11, 2004, 13:01:12 ; Search time 7.61905 Seconds
(without alignments)
68.342 Million cell updates/sec

le: US-10-661-207-1
fect score: 47
ence: 1 GPCXXFYRY 10

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 141681 seqs, 52070155 residues

l number of hits satisfying chosen parameters: 141681

imum DB seq length: 0
imum DB seq length: 2000000000

rocessing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ibase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| alt no. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|----------------|--------|----|------------|---------------------|
| 1 | 42 | 89.4 | 122 | 1 | UPTI_PIG | Q29100 sus scrofa |
| 2 | 37 | 78.7 | 25 | 1 | BT14_BOOMI | P83605 boophilus m |
| 3 | 37 | 78.7 | 60 | 1 | IBPS_BOVIN | P00975 bos taurus |
| 4 | 37 | 78.7 | 133 | 1 | EPPI_MACMU | Q9bd11 macaca mula |
| 5 | 36 | 76.6 | 100 | 1 | BPTI_BOVIN | P00974 bos taurus |
| 6 | 36 | 76.6 | 100 | 1 | BPT2_BOVIN | P04815 bos taurus |
| 7 | 35 | 74.5 | 55 | 1 | CSTI_BOMMO | P81902 bombyx mori |
| 8 | 35 | 74.5 | 61 | 1 | IBPI_TACTR | P16044 tachypleus |
| 9 | 35 | 74.5 | 62 | 1 | IP52_ANESU | P10280 anemonia su |
| 10 | 35 | 74.5 | 67 | 1 | IBPC_BOVIN | P00976 bos taurus |
| 11 | 35 | 74.5 | 197 | 1 | MCPI_MELCP | P82988 melithaea c |
| 12 | 35 | 74.5 | 330 | 1 | RFBI_SALTY | P26395 salmonella |
| 13 | 34 | 72.3 | 123 | 1 | IATR_SHEEP | P13371 ovis aries |
| 14 | 34 | 72.3 | 235 | 1 | TFP2_HUMAN | P48307 homo sapien |
| 15 | 34 | 72.3 | 352 | 1 | AMBP_BOVIN | P00978 bos taurus |
| 16 | 34 | 72.3 | 361 | 1 | HALU_MOUSE | P14433 mus musculus |
| 17 | 34 | 72.3 | 384 | 1 | HALT_MOUSE | P14432 mus musculus |
| 18 | 33 | 70.2 | 53 | 1 | HTIB_MANSE | P26227 manduca sex |
| 19 | 32 | 68.1 | 56 | 1 | ITRA_RADMA | P16344 radianthus |
| 20 | 32 | 68.1 | 58 | 1 | ISIK_HELPO | P00994 helix pomat |
| 21 | 32 | 68.1 | 470 | 1 | EXON_EBV | P03217 Epstein-bar |
| 22 | 32 | 68.1 | 883 | 1 | SYA_EUCAP | O8k9e7 buchnera ap |
| 23 | 32 | 68.1 | 1544 | 1 | TULA_HUMAN | Q9nr14 homo sapien |
| 24 | 32 | 68.1 | 1547 | 1 | TUL4_MOUSE | Q9j115 mus musculus |
| 25 | 31 | 66.0 | 252 | 1 | SPT2_HUMAN | O43291 homo sapien |
| 26 | 31 | 66.0 | 252 | 1 | SPT2_MOUSE | Q9wu03 mus musculus |
| 27 | 31 | 66.0 | 370 | 1 | AAT2_METJA | O58097 methanococc |
| 28 | 31 | 66.0 | 701 | 1 | ACSA_HUMAN | Q9nr19 homo sapien |
| 29 | 31 | 66.0 | 989 | 1 | SERA_PLAEG | P13823 plasmodium |
| 30 | 31 | 66.0 | 2127 | 1 | RRPL_RAEVS | P16289 rabies viru |
| 31 | 30 | 63.8 | 133 | 1 | EPPI_HUMAN | Q95925 homo sapien |
| 32 | 30 | 63.8 | 201 | 1 | SYA_RHLIV | P24075 rhizobium l |
| 33 | 30 | 63.8 | 310 | 1 | OK4E_HUMAN | Q8ngd5 homo sapien |

ALIGNMENTS

RESULT 1

| ID | UPTI_PIG | STANDARD; | PRT; | 122 AA. |
|------|--|-----------|------|------------------------------------|
| AC | Q29100; | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 15-MAR-2004 (Rel. 43, Last annotation update) | | | |
| DE | Uterine plasmin/trypsin inhibitor precursor (UPTI). | | | |
| OS | Sus scrofa (Pig). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. | | | |
| OX | NCBI_TaxID=9823; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A., SEQUENCE OF 30-56, AND CHARACTERIZATION. | | | |
| RC | TISSUE=Conceptus membranes, and Uterus; | | | |
| RX | MEDLINE=9501440; PubMed=7929061; | | | |
| RA | Stallings-Wann M.L., Burke M.G., Trout W.E., Roberts R.M.; | | | |
| RT | "Purification, characterization, and cDNA cloning of a Kunitz-type | | | |
| RT | proteinase inhibitor secreted by the porcine uterus."; | | | |
| RL | J. Biol. Chem. 269:24090-24094(1994). | | | |
| CC | -!- FUNCTION: Inhibitor of plasmin and trypsin. Also has a weak | | | |
| CC | affinity for chymotrypsin. Could serves to neutralize the | | | |
| CC | activities of one or more serine proteinases generated by the | | | |
| CC | proliferating trophoblast during the formation of the noninvasive | | | |
| CC | placenta. | | | |
| CC | -!- TISSUE SPECIFICITY: Expressed only in the uterus and the | | | |
| CC | endometrium. | | | |
| CC | -!- DEVELOPMENTAL STAGE: Maximally expressed during pregnancy until | | | |
| CC | day 30 after which levels decrease significantly. | | | |
| CC | -!- INDUCTION: By progesterone. | | | |
| CC | -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain. | | | |
| CC | ----- | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| EMBL | LI4282; AAG62425.1; - | | | |
| DR | PIR; A55115; A55115. | | | |
| DR | HSSP; P00974; 1BPI. | | | |
| DR | InterPro; IPR002223; Kunitz_BPTI. | | | |
| DR | Pfam; PF00014; Kunitz_BPTI_1. | | | |
| DR | PRINTS; PR00759; BASICPTASE. | | | |
| DR | ProDom; PD000222; Kunitz_BPTI; 1. | | | |
| DR | SMART; SM00131; KU; 1. | | | |
| DR | PROSITE; PS00280; BPTI_KUNITZ_1; 1. | | | |
| DR | PROSITE; PS02079; BPTI_KUNITZ_2; 1. | | | |
| KW | Serine protease inhibitor; Signal. | | | |
| FT | SIGNAL 1 20 POTENTIAL. | | | |
| FT | PROPEP 21 29 | | | |
| FT | CHAIN 30 122 | | | |
| FT | DOMAIN 38 88 | | | |
| FT | DISULFID 38 88 | | | |
| | | | | UTERINE PLASMIN/TRYPsin INHIBITOR. |
| | | | | BPTI/KUNITZ INHIBITOR. |
| | | | | BY SIMILARITY. |

P57483 buchnera ap
P59420 buchnera ap
Q98nq5 rhizobium l
P28962 equine herp
P26226 manduca sex
O43715 homo sapien
Q9d822 mus musculus
P04365 equus caball
Q07549 saccharomyc
Q43646 solanum tub
Q9a9x1 caulobacter
Q8nh73 homo sapien

1 SYA_BUCAL
1 SYA_BUCBP
1 SYA_RHLIO
1 UL52_HSVEB
1 HTIA_MANSE
1 15E1_HUMAN
1 15E1_MOUSE
1 IATR_HORSE
1 YD23_YEAST
1 API2_SOLITU
1 UBIG_CAUCR
1 O482_HUMAN

30 63.8
30 63.8
30 63.8
30 63.8
29 61.7
29 61.7
29 61.7
29 61.7
29 61.7
29 61.7
29 61.7
29 61.7
29 61.7

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FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT CONFLICT 36 36 G -> A (IN REF. 1; AA SEQUENCE).
FT CONFLICT 48 48 S -> R (IN REF. 1; AA SEQUENCE).
FT CONFLICT 52 52 V -> I (IN REF. 1; AA SEQUENCE).
FT CONFLICT 54 54 Y -> V (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 122 AA; 1310 MW; B9BEFB3A6FB76CEC CRC64;

Query Match 89.4%; Score 42; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 0.019;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPCXXXPIRY 10
Db 45 GPCSAHFVRY 54

RESULT 2
BT14_BOOMI
ID BT14_BOOMI STANDARD; PRT; 25 AA.
AC P83605;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kunitz-type serine protease inhibitor BmtI-4 (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Larva.
RA Sasaki S.D., Hirata I.Y., Tanaka A.S.;
RT "Molecular studies of serine protease inhibitors from cattle tick
  Boophilus microplus (larvae).";
RL Submitted (JUN-2003) to Swiss-Prot.
CC -!- FUNCTION: Inhibits trypsin, human plasma kallikrein and human
  neutrophil elastase.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR InterPro; IPR002223; Kunitz_BPTI.
DR PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
DR PROSITE; PS02079; BPTI_KUNITZ_2; PARTIAL.
KW Serine protease inhibitor.
FT ACT SITE 18 19 REACTIVE BOND (BY SIMILARITY).
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2963 MW; 81CB3A2D2E121F3D CRC64;

Query Match 78.7%; Score 37; DB 1; Length 25;
Best Local Similarity 60.0%; Pred. No. 0.051;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXPIRY 10
Db 15 GPCVGYFFRY 24

RESULT 3
IBPS_BOVIN
ID IBPS_BOVIN STANDARD; PRT; 60 AA.
AC P00975;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum basic protease inhibitor (Serum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.

```

```

RX MEDLINE=81044408; PubMed=7428928;
RA Wachter E., Deppner K., Hochstrasser K., Lempart K., Geiger R.;
RT "A new Kunitz-type inhibitor from bovine serum amino acid sequence
  determination.";
RL FEBS Lett. 119:58-62(1980).
CC -!- FUNCTION: This inhibitor has activity very similar to that of the
  basic protease inhibitor from bovine tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01206; TIBOR.
DR HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PD00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57 BY SIMILARITY.
FT DISULFID 16 40 BY SIMILARITY.
FT DISULFID 32 53 BY SIMILARITY.
FT ACT SITE 17 18 REACTIVE BOND.
SQ SEQUENCE 60 AA; 6647 MW; B9953EBAACFLA4E6 CRC64;

Query Match 78.7%; Score 37; DB 1; Length 60;
Best Local Similarity 60.0%; Pred. No. 0.12;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXPIRY 10
Db 14 GPCKAAMIRY 23

RESULT 4
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
  inhibitor-like with Kunitz and WAP domains 1).
GN SPINUM1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.;
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
  epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346414; AAK31336.1; -.
DR HSSP; P00974; 1BPI.
DR InterPro; IPR002223; Kunitz_BPTI.

```


InterPro: IPR008197; WAP.
 Pfam: PF00014; Kunitz_BPTI; 1.
 Pfam: PF00035; wap; 1.
 PRINTS: PR00759; BASICPTASE.
 ProDom: PD00022; Kunitz_BPTI; 1.
 SMART: SM00131; KUP; 1.
 SMART: SM0217; WAP; 1.
 PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 Serine protease inhibitor; Signal.
 SIGNAL 1 21 POTENTIAL.
 CHAIN 22 133 EPPIN.
 DOMAIN 29 73 WAP.
 DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
 DISULFID 33 61 BY SIMILARITY.
 DISULFID 40 65 BY SIMILARITY.
 DISULFID 48 60 BY SIMILARITY.
 DISULFID 54 69 BY SIMILARITY.
 DISULFID 77 127 BY SIMILARITY.
 DISULFID 86 110 BY SIMILARITY.
 DISULFID 102 123 BY SIMILARITY.
 SEQUENCE 133 AA; 433AE946E39A35E9 CRC64;

very Match 78.7%; Score 37; DB 1; Length 133;
 1st Local Similarity 60.0%; Pred. No. 0.27;
 itches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 GPCXXXPYR 10
 ||| |||
 84 GPCIAFPYR 93

ILT 5

BPTI_BOVIN STANDARD; PRT; 100 AA.
 P00974;
 21-JUL-1986 (Rel. 10, Last created)
 01-MAR-1989 (Rel. 10, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Pancreatic trypsin inhibitor precursor (Basic protease inhibitor)
 (BPI) (BPTI) (Aprotinin).
 Bos taurus (Bovine).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=87283904; PubMed=2441071;
 Creighton T.E., Charles I.G.;
 "Sequences of the genes and polypeptide precursors for two bovine
 protease inhibitors.";
 J. Mol. Biol. 194:11-22(1987).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=8295740; PubMed=2456884;
 Creighton T.E., Charles I.G.;
 "Biosynthesis, processing, and evolution of bovine pancreatic trypsin
 inhibitor.";
 Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).
 [3]
 SEQUENCE OF 34-97 FROM N.A.
 MEDLINE=86158754; PubMed=2420326;
 Kingston I.B., Anderson S.;
 "Sequences encoding two trypsin inhibitors occur in strikingly
 similar genomic environments.";
 Biochem. J. 233:443-450(1986).
 [4]
 SEQUENCE OF 34-97 FROM N.A.
 MEDLINE=84070725; PubMed=6580617;
 Anderson S., Kingston I.B.;
 "Isolation of a genomic clone for bovine pancreatic trypsin inhibitor
 by using a unique-sequence synthetic DNA probe.";

RL Proc. Natl. Acad. Sci. U.S.A. 80:6838-6842(1983).
 RN [5]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66083012; PubMed=5860161;
 RA Kassell B., Laskowski M.;
 RT "The basic trypsin inhibitor of bovine pancreas. V. The disulfide
 linkages.";
 RL Biochem. Biophys. Res. Commun. 20:463-468(1965).
 RN [6]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=66171231; PubMed=5296424;
 RA Anderer F.A., Hornle S.;
 RT "The disulfide linkages in kallikrein inactivator of bovine lung.";
 J. Biol. Chem. 241:1568-1572(1966).
 RN [7]
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.
 RX MEDLINE=68012003; PubMed=6053284;
 RA Chauvet J., Acher R.;
 RT "Covalent structure of a polypeptide inhibitor of trypsin (Kunitz and
 Northrop inhibitor).";
 Bull. Soc. Chim. Biol. 49:985-1000(1967).
 RN [8]
 RP SEQUENCE OF 36-93.
 RA Dlouha V., Pospisilova D., Meloun B., Sorm F.;
 RT "Sequence of residues 18-20 in pancreatic trypsin inhibitor.";
 Collect. Czech. Chem. Commun. 33:1363-1365(1968).
 RN [9]
 RP SEQUENCE OF 36-81.
 RC TISSUE=Adrenal chromaffin;
 RX MEDLINE=90211226; PubMed=2322242;
 RA Lewis R.V., Ray P., Coghill R., Krugel W.;
 RT "Presence of pancreatic trypsin inhibitor in adrenal medullary
 chromaffin cells.";
 Biochem. Biophys. Res. Commun. 167:543-547(1990).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA Deisenhofer J., Steigemann W.;
 RT "Crystallographic refinement of the structure of bovine pancreatic
 trypsin inhibitor at 1.5-A resolution.";
 Acta Crystallogr. B 31:238-250(1975).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=70255230; PubMed=5447861;
 RA Huber R., Kukla D., Ruhlmann A., Epp O., Formanek H.;
 RT "The basic trypsin inhibitor of bovine pancreas. I. Structure
 analysis and conformation of the polypeptide chain.";
 Naturwissenschaften 57:389-392(1970).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.
 RX MEDLINE=91332906; PubMed=1714504;
 RA Housset D., Kim K.-S., Fuchs J., Woodward C., Wlodawer A.;
 RT "Crystal structure of a Y35G mutant of bovine pancreatic trypsin
 inhibitor.";
 J. Mol. Biol. 220:757-770(1991).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93021116; PubMed=1383552;
 RA Berndt K.D., Guntert P., Orbons L.P.M., Wuthrich K.;
 RT "Determination of a high-quality nuclear magnetic resonance solution
 structure of the bovine pancreatic trypsin inhibitor and comparison
 with three crystal structures.";
 J. Mol. Biol. 227:757-775(1992).
 RL CC -1- FUNCTION: Inhibits trypsin, kallikrein, chymotrypsin, and plasmin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PHARMACOLOGICAL: Available under the name Trasylol (Mile). Used
 CC for inhibiting coagulation so as to reduce blood loss during
 CC bypass surgery.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -1- DATABASE: NAME=Trasylol; NOTE=Clinical information on Trasylol;
 CC WWW="http://www.trasylol.com/".

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[6]
SEQUENCE OF 36-93 (SI-II).
MEDLINE=86008178; PubMed=2413011;
Fioretto E., Iacopino G., Angeletti M., Barra D., Bossa F., Ascoli F.;
"Primary structure and antiproteolytic activity of a Kunitz-type
inhibitor from bovine spleen.";
J. Biol. Chem. 260:11451-11455(1985).
[7]
SEQUENCE OF 36-97 (SI-III).
MEDLINE=91098258; PubMed=1986787;
Barra D., Fioretto E., Angeletti M., Barra D., Bossa F., Ascoli F.;
"Proteinase inhibitors from bovine spleen: primary structure of an
intermediate in the processing of the precursor.";
Biochim. Biophys. Acta 1076:143-147(1991).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M20935; AAA51418.1; --
EMBL; M20931; AAA51418.1; JOINED.
EMBL; M20933; AAA51418.1; JOINED.
EMBL; X05275; CAA28887.1; --
EMBL; X06685; CAA29881.1; --
EMBL; X03366; CAA27064.1; ALT_SEQ.
EMBL; X03366; CAA27065.1; --
PIR; S00274; TIBOSP.
HSSP; P00974; IBPI.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SW00131; KU; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS0279; BPTI_KUNITZ_2; 1.
Serine protease inhibitor; Signal.
SIGNAL 1 21 POTENTIAL.
PROPEP 22 33 SPLEEN TRYPSIN INHIBITOR I.
CHAIN 34 99 SPLEEN TRYPSIN INHIBITOR II.
CHAIN 36 93 SPLEEN TRYPSIN INHIBITOR III.
CHAIN 36 97 BPTI/KUNITZ INHIBITOR.
DOMAIN 40 90 BY SIMILARITY.
DISULFID 40 90 BY SIMILARITY.
DISULFID 49 73 BY SIMILARITY.
DISULFID 65 86 BY SIMILARITY.
ACT_SITE 50 51 REACTIVE_BOND (BY SIMILARITY).
SEQUENCE 100 AA; 10843 MW; 39069734B8ACF4E3 CRC64;
ery Match 76.6%; Score 36; DB 1; Length 100;
st Local Similarity 60.0%; Pred. No. 0.33;
tches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GPCXXXPYRY 10
||| |||
47 GPCXKMYRY 56
LT 7
-BOMMO STANDARD; PRT; 55 AA.
P81902;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RC SEQUENCE, AND CHARACTERIZATION.
RX STRAIN=Asahi;
RC MEDLINE=99115431; PubMed=9914483;
RA Kurioka A., Yamazaki M., Hirano H.;
RT Bombyx mori.;
RT Primary structure and possible functions of a trypsin inhibitor of
Bombyx mori.;
RL Eur. J. Biochem. 259:120-126(1999).
CC -!- FUNCTION: This cocoon shell-associated protein inhibits trypsin
activity by forming a low-dissociation complex with trypsin. May
play an important part in regulating proteolytic activity in the
silk gland or protecting silk proteins from degradation during
histolysis.
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
gland.
CC -!- DEVELOPMENTAL STAGE: Expression differentially regulated in the
middle silk glands during the final stage of larval growth with
highest expression before the onset of spinning.
CC -!- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray.
CC -!- MISCELLANEOUS: Has an isoelectric point of 4.3.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SW00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Developmental protein; Serine protease inhibitor.
FT DISULFID 4 54 BY SIMILARITY.
FT DISULFID 13 37 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT ACT_SITE 14 15 REACTIVE_BOND (TRYPSIN) (BY
SIMILARITY).
FT SEQUENCE 55 AA; 6027 MW; C2739BB8F2BB6E59 CRC64;
Query Match 74.5%; Score 35; DB 1; Length 55;
Best Local Similarity 60.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPCXXXPYRY 10
||| |||
DB 11 GPCXGSPYRY 20
RESULT 8
IBPI_TACTR
ID IBPI_TACTR STANDARD; PRT; 61 AA.
AC P16044;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proteinase inhibitor (BPI-type).
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemocyte;
RX MEDLINE=88007472; PubMed=3308864;
RA Nakamura T., Hirai T., Tokunaga F., Kawabata S., Iwanaga S.;
RT "Purification and amino acid sequence of Kunitz-type protease
inhibitor found in the hemocytes of horseshoe crab (Tachypleus
tridentatus).";
RT J. Biochem. 101:1297-1306(1987).
RL J. Biochem. 101:1297-1306(1987).
CC -!- FUNCTION: Inhibitor of trypsin and chymotrypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A26923; THICBP.
 DR HSSP; P00974; IBPI.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 8 58 BY SIMILARITY.
 FT DISULFID 17 41 BY SIMILARITY.
 FT DISULFID 33 54 BY SIMILARITY.
 FT ACT SITE 18 19 REACTIVE BOND (BY SIMILARITY).
 SQ SEQUENCE 61 AA; 6825 MW; 730E82CDD0653E48 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 61;
 Best Local Similarity 60.0%; Pred. No. 0.34;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXPIRY 10
 ||| |||
 DB 15 GPCRAQPKRY 24

RESULT 9

IP52 ANESU STANDARD; PRT; 62 AA.
 AC P10280; 1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protease inhibitor 5 II (SA5 II).
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anemonia.
 OC NCBI_TaxID=6108;
 RN [1]
 RP SEQUENCE OF 1-59.
 RA Wunderer G., Machleidt W., Fritz H.;
 FT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 RT Anemonia sulcata.";
 RL Meth. Enzymol. 80:816-820(1981).
 RN [2]

SEQUENCE.
 RA Krebs H.C., Habermehl G.G.;
 RT "Isolation and structural determination of a hemolytic active peptide
 from the sea anemone Metridium senile.";
 RL Naturwissenschaften 74:395-396(1987).
 CC -1- FUNCTION: Inhibitor of kallikreins.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S07451; S07451.
 DR HSSP; P31713; LSHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.

FT DISULFID 5 55 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT ACT SITE 15 16 REACTIVE BOND (BY SIMILARITY).
 FT VARIANT 13 13 P -> R.
 FT VARIANT 16 16 A -> G.
 FT VARIANT 17 17 R -> G.
 FT VARIANT 25 25 S -> L.
 FT VARIANT 28 28 K -> R.
 FT VARIANT 39 39 G -> R.
 SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 62;
 Best Local Similarity 60.0%; Pred. No. 0.35;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXPIRY 10
 ||| |||
 DB 12 GPCRAQPKRY 21

RESULT 10

IBPC BOVIN STANDARD; PRT; 67 AA.
 AC P00976;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Colostrum trypsin inhibitor (Colostrum BPI).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Cechova D., Jonakova V., Sorm F.;
 RT "Primary structure of trypsin inhibitor from cow colostrum (component
 RT B2).";
 RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
 RN [2]
 RP DISULFIDE BONDS.
 RA Cechova D., Ber E.;
 RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
 RL Collect. Czech. Chem. Commun. 39:680-688(1974).
 RN [3]

CHARACTERIZATION.
 RA Cechova D., Muszynska G.;
 RT "Role of lysine 18 in active center of cow colostrum trypsin
 RT inhibitor.";
 RL FEBS Lett. 8:84-86(1970).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; A01207; TIBOC.
 DR HSSP; P02760; LBIK.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Glycoprotein.

FT DISULFID 8 58
 FT DISULFID 17 41
 FT DISULFID 33 54
 FT CARBOHYD 27 27
 FT ACT SITE 18 19
 SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 74.5%; Score 35; DB 1; Length 67;
 Best Local Similarity 50.0%; Pred. No. 0.38;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXPIRY 10
 ||| |||
 DB 15 GPCXAALRY 24

RESULT 11
 MCP1_MELCP STANDARD; PRT; 197 AA.
 ID MCP1_MELCP
 AC P82968;
 DT 28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Protease inhibitor (McpA).
 Melithaea caledonica.
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Gorgonacea;
 Scleraxonia; Melithaeidae; Melithaea.
 NCBI_TaxID=156534;
 [1]
 SEQUENCE, AND VARIANT VAL-195.
 Peduzzi J., Longeon A., Guyot M., Barthelemy M.;
 "Amino acid sequence and kinetic properties of a four-domain proteases
 inhibitor from the gorgonian Melithaea caledonica";
 Eur. J. Biochem. 0:0-0(2001).
 -1- FUNCTION: INHIBITS TRYPSIN, KALLIKREIN, SUBTILISIN CARLSBERG,
 HUMAN LEUKOCYTE ELASTASE, PORCINE PANCREATIC ELASTASE AND
 CHYMOTRYPSIN. TWO DOMAINS ARE FOR THE INHIBITION OF CHYMOTRYPSIN.
 -1- SIMILARITY: Contains 3 Kazal-like domains.
 -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 HSP; P31713; ISHP.
 InterPro; IPR002350; Kazal.
 InterPro; IPR002223; Kunitz_BPTI.
 Pfam; PF00050; kazal; 3.
 PRINTS; PR00759; BASICPTASE.
 PRODOM; PD000222; Kunitz_BPTI; 1.
 SMART; SM00131; KU; 1.
 PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 PROSITE; PS00282; KAZAL; FALSE_NEG.
 Serine protease inhibitor; Repeat.
 DOMAIN 1 45 KAZAL-LIKE 1.
 DOMAIN 49 93 KAZAL-LIKE 2.
 DOMAIN 97 141 KAZAL-LIKE 3.
 DOMAIN 144 194 BPTI/KUNITZ INHIBITOR.
 ACT_SITE 7 8 REACTIVE BOND 1 (BY SIMILARITY).
 ACT_SITE 55 56 REACTIVE BOND 2 (BY SIMILARITY).
 ACT_SITE 103 104 REACTIVE BOND 3 (BY SIMILARITY).
 ACT_SITE 154 155 REACTIVE BOND 4 (BY SIMILARITY).
 DISULFID 1 31 BY SIMILARITY.
 DISULFID 5 24 BY SIMILARITY.
 DISULFID 13 45 BY SIMILARITY.
 DISULFID 49 79 BY SIMILARITY.
 DISULFID 53 72 BY SIMILARITY.
 DISULFID 61 93 BY SIMILARITY.
 DISULFID 97 127 BY SIMILARITY.
 DISULFID 101 120 BY SIMILARITY.
 DISULFID 109 141 BY SIMILARITY.
 DISULFID 144 194 BY SIMILARITY.
 DISULFID 153 177 BY SIMILARITY.
 DISULFID 169 190 BY SIMILARITY.
 VARIANT 195 195 M -> V.
 SEQUENCE 197 AA; 21248 MW; 199D08A489879579 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 197;
 Best Local Similarity 60.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFYRY 10
 |||||
 151 GPCRGAFRY 160

LT 12

SALTY
 RPBI SALTY STANDARD; PRT; 330 AA.
 P2635;
 01-AUG-1992 (Rel. 23, Created)
 01-AUG-1992 (Rel. 23, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Rfbi protein.
 RPBI OR STM2093
 Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RC MEDLINE=91260454; PubMed=1710759;
 RA Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
 RT "Structure and sequence of the rfb (O antigen) gene cluster of
 RT Salmonella serovar typhimurium (strain LT2).";
 RL Mol. Microbiol. 5:695-713(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 CC -1- PATHWAY: Lipopolysaccharide O antigen biosynthesis.
 CC -----
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 CC -----
 CC EMBL; X56793; CAA40119.1; --
 DR EMBL; AE008792; AAL20997.1; --
 DR DDB; S15303; S15303.
 DR HSP; P00235; IFRR.
 DR StyGene; SG10451; rfbI.
 DR InterPro; IPR006058; 2Fe2S fd BS.
 DR InterPro; IPR008333; PAD binding_6.
 DR InterPro; IPR001041; Ferridoxin.
 DR InterPro; IPR001709; FPN_cyt_redctase.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR PRINTS; PR00371; PFNCR.
 DR PRINTS; PR00410; PHEHYDRYLASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; Complete proteome.
 KW Lipopolysaccharide biosynthesis; Complete proteome.
 SQ SEQUENCE 330 AA; 36582 MW; EFC1BEC17A0CC82D CRC64;

Query Match 74.5%; Score 35; DB 1; Length 330;
 Best Local Similarity 66.7%; Pred. No. 1.8;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GPCXXXFYR 9
 |||||
 DB 184 GPCGTFYR 192

RESULT 13

IATR SHEEP
 ID IATR SHEEP STANDARD; PRT; 123 AA.
 AC P13371;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of
 DE ITI) (Fragment).
 OS Ovis aries (Sheep), and
 OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940, 9925;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Sheep;
 RX MEDLINE=8729012; PubMed=2441725;
 RA Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.;
 RT "The amino-acid sequence of the trypsin-released inhibitor from sheep
 inter-alpha-trypsin inhibitor.";
 RL Biol. Chem. Hoppe-Seyler 368:727-731(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.hircus;
 RX MEDLINE=90105540; PubMed=2481505;
 RA Rasp G., Hochstrasser K., Gerl C., Wachter E.;
 RT "Primary structure of a proteinase inhibitor released from goat serum
 inter-alpha-trypsin inhibitor.";
 RL Biochim. Biophys. Acta 999:335-337(1989).
 CC -!- FUNCTION: This inhibitory fragment, released from native ITI after
 limited proteolysis with trypsin, contains two homologous domains.
 CC Whereas the second domain is a strong inhibitor of trypsin, the
 CC first domain interacts weakly with PMN-granulocytic elastase and
 CC not at all with pancreatic elastase.
 CC -!- MISCELLANEOUS: The amino acid at position p2' (17) appears to
 CC determine the specificity of the inhibition of domain I.
 CC Inhibitors with methionine in this position interact weakly with
 CC chymotrypsin and elastase; those with leucine interact strongly.
 CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR PIR: A29652; A29652.
 DR HSP: P02760, 18IK.
 DR InterPro: IPR002223; Kunitz BPTI.
 DR Pfam: PF00014; Kunitz BPTI; 2.
 DR PRINTS: PR00759; BASICTPASE.
 DR ProDom: PD000222; Kunitz_BPTI; 2.
 DR SMART: SM00131; KU; 2.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE: PS02079; BPTI_KUNITZ_2; 2.
 DR Plasma: Glycoprotein; Serine protease inhibitor; Repeat.
 FT NON TER 1 1 BPTI/KUNITZ INHIBITOR 1.
 FT DOMAIN 5 55 BPTI/KUNITZ INHIBITOR-2.
 FT DISULFID 61 111 BY SIMILARITY.
 FT DISULFID 14 38 BY SIMILARITY.
 FT DISULFID 30 51 BY SIMILARITY.
 FT DISULFID 61 111 BY SIMILARITY.
 FT DISULFID 70 94 BY SIMILARITY.
 FT DISULFID 86 107 BY SIMILARITY.
 FT SITE 15 16 INHIBITORY (PI) (CHYMOTRYPSIN, ELASTASE).
 FT SITE 71 72 INHIBITORY (PI) (TRYPSIN).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .).
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13686 MW; 295038173F22D2D1 CRC64;
 Query Match 72.3%; Score 34; DB 1; Length 123;
 Best Local Similarity 60.08; Pred. No. 1-1;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GPCXXXFYRY 10
 Db 12 GPCLGMPKRY 21
 RESULT 14
 TFP2 HUMAN STANDARD; PRT; 235 AA.
 ID TFP2 HUMAN
 AC P48307;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue factor pathway inhibitor 2 precursor (TFPI-2) (Placental
 protein 5) (pp5).
 DB

GN TFP12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=95204397; PubMed=7896752;
 RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F.,
 RA Aoki I., Misugi K., Umeda M., Miyazaki K.;
 RT "cDNA cloning and mRNA expression of a serine proteinase inhibitor
 secreted by cancer cells: identification as placental protein 5 and
 tissue factor pathway inhibitor-2.";
 RL J. Biochem. 116:939-942(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94211862; PubMed=8159751;
 RA Sprecher C.A., Kiesel W., Mathewes S., Foster D.C.;
 RT "Molecular cloning, expression, and partial characterization of a
 second human tissue-factor-pathway inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Maggi L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21240334; PubMed=11342222;
 RA Kamei S., Kazama Y., Kuiper J.L., Foster D.C., Kiesel W.;
 RT "Genomic structure and promoter activity of the human tissue factor
 pathway inhibitor-2 gene.";
 RL Biochim. Biophys. Acta 1517:430-435(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Launser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Abramson R.D., Mullaby S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalek U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
 RC TISSUE=Placenta;
 RX MEDLINE=88106628; PubMed=3276312;
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppäläe M.;
 RT "Purification and characterization of placental protein 5.";
 RL Biochem. Biophys. Res. Commun. 150:483-490(1988).
 RN [7]
 RP ERRATUM.
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppäläe M.;
 RL Biochem. Biophys. Res. Commun. 151:630-631(1988).
 CC -!- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,
 CC weakly factor Xa. Has no effect on thrombin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,

placenta, heart, pancreas, and maternal serum at advanced pregnancy.

-!- DOMAIN: This inhibitor contains three inhibitory domains.

-!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.

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EMBL; D29992; BAA06272.1; --
EMBL; L27624; AAA20094.1; --
EMBL; AC02076; --; NOT ANNOTATED_CDS.
EMBL; AF217542; AK13254.1; --
EMBL; BC065330; AA05330.1; --
PIR; A54951; A54951.
HSSP; P12111; 1KNT.
Genew; HGNC:11761; TFP12.
MIM; 600033; --
GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
InterPro; IPR022223; Kunitz_BPTI.
InterPro; IPR008296; TFP1.
Pfam; PF00014; Kunitz_BPTI; 3.
PIRSF; PIRSF001620; TFP1; 1.
PRINTS; PR00759; BASICTPASE.
ProDom; PD000222; Kunitz_BPTI; 3.
SMART; SM00131; KU; 3.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS0279; BPTI_KUNITZ_3; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Signal;
Blood coagulation; Polymorphism.

SIGNAL 1 23 TISSUE FACTOR PATHWAY INHIBITOR 2.

CHAIN 23 235 BPTI/KUNITZ INHIBITOR 1.

DOMAIN 36 86 BPTI/KUNITZ INHIBITOR 2.

DOMAIN 158 208 BPTI/KUNITZ INHIBITOR 3.

DOMAIN 213 217 POLY-LYS.

ACT_SITE 46 47 REACTIVE BOND (BY SIMILARITY).

ACT_SITE 107 108 REACTIVE BOND (BY SIMILARITY).

ACT_SITE 168 169 REACTIVE BOND (BY SIMILARITY).

DISULFID 36 86 BY SIMILARITY.

DISULFID 45 69 BY SIMILARITY.

DISULFID 61 82 BY SIMILARITY.

DISULFID 96 149 BY SIMILARITY.

DISULFID 106 130 BY SIMILARITY.

DISULFID 122 145 BY SIMILARITY.

DISULFID 158 208 BY SIMILARITY.

DISULFID 167 191 BY SIMILARITY.

DISULFID 183 204 BY SIMILARITY.

CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).

VARIANT 102 102 V -> A (in GDSNP:1804202).

CONFLICT 23 23 D -> A (in REF. 6).

SEQUENCE 235 AA; 26934 MW; 975ABA5C3F7C65F CRC64;

72.3%; Score 34; DB 1; Length 235;

Local Similarity 50.8%; Pred. No. 2.2;

5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFYIR 10

||| :||

43 GPCRALLYR 52

LT 15

BOVIN

AMBP BOVIN STANDARD; PRT; 352 AA.

P00978; P35420; Q28020;

DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (BI-14)
(Cumulus extracellular matrix stabilizing factor) (ESF)].
DE AMBP OR ITIL.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96201710; PubMed=8611630;
RA Lindqvist A., Aakerstroem B.;
RT "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization
of liver cDNA and urinary alpha 1-microglobulin.";
RL Biochim. Biophys. Acta 1306:98-106(1996).
RN [2]
RP SEQUENCE OF 227-349.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
trypsin-released inhibitors from horse and pig inter-alpha-trypsin
inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
RN [3]
RP SEQUENCE OF 227-348.
RX MEDLINE=84133807; PubMed=6199275;
RA Hochstrasser K., Wachter E.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor, VII. Determination of the
amino-acid sequence of the trypsin-released inhibitor from bovine
inter-alpha-trypsin inhibitor.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
RN [4]
RP SEQUENCE OF 206-219.
RX TISSUE=Fetal serum;
MEDLINE=92291130; PubMed=1376324;
Chen L., Mao S.J.T., Larsen W.J.;
RT "Identification of a factor in fetal bovine serum that stabilizes the
cumulus extracellular matrix. A role for a member of the inter-alpha-
trypsin inhibitor family.";
RL J. Biol. Chem. 267:12380-12386(1992).
RN [5]
RP REACTIVE SITES.
RX MEDLINE=84133808; PubMed=6199276;
RA Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor, VII. Characterization of the
bovine inhibitor as double-headed trypsin-elastase inhibitor.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
AND ALBUMIN.
CC -!- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
urine, inhibits trypsin, plasmin, and lysosomal granulocytic
elastase.
CC -!- FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY
STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS
EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR
MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.
CC -!- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from
one or two heavy chains (H1, H2 or H3) and one light chain,
bikunin. Inter-alpha-inhibitor (I-alpha-1) is composed of H1, H2
and bikunin, inter-alpha-like inhibitor (I-alpha-Li) of H2 and
bikunin, and pre-alpha-inhibitor (P-alpha-1) of H3 and bikunin (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.

Search completed: August 11, 2004, 13:08:06
Job time : 8.61905 secs

CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-
CC yellow chromophores (By similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -----
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CC -----
DR EMBL; U35642; AAB07599.1; --
DR PIR; S68149; TIBOBI.
DR HSP; P02760; IBIK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00014; Kunitz_BPTI_2.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00759; BASICTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR ProDom; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW Lipocalin.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 203 ALPHA-1 MICROGLOBULIN.
FT CHAIN 206 352 INTER-ALPHA-TRYPsin INHIBITOR LIGHT
FT CHAIN CHAIN.
FT DOMAIN 231 281 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 287 337 BPTI/KUNITZ INHIBITOR 2.
FT BINDING 53 53 CHROMOPHORE (BY SIMILARITY).
FT BINDING 111 111 CHROMOPHORE (BY SIMILARITY).
FT BINDING 137 137 CHROMOPHORE (BY SIMILARITY).
FT BINDING 149 149 CHROMOPHORE (BY SIMILARITY).
FT DISULFID 91 188 BY SIMILARITY.
FT DISULFID 231 281 BY SIMILARITY.
FT DISULFID 240 264 BY SIMILARITY.
FT DISULFID 256 277 BY SIMILARITY.
FT DISULFID 287 337 BY SIMILARITY.
FT DISULFID 296 320 BY SIMILARITY.
FT DISULFID 312 333 BY SIMILARITY.
FT SITE 241 242 INHIBITORY (P1) (CHYMOTRYPSIN, ELASTASE).
FT SITE 297 298 INHIBITORY (P1) (TRYPSIN).
FT SITE 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 209 209 T -> G (IN REF. 4).
FT CONFLICT 217 217 A -> D (IN REF. 4).
FT CONFLICT 268 268 G -> L (IN REF. 2 AND 3).
FT CONFLICT 274 274 E -> Q (IN REF. 2 AND 3).
FT CONFLICT 298 299 SY -> AF (IN REF. 2 AND 3).
FT CONFLICT 330 330 E -> Q (IN REF. 2 AND 3).
FT CONFLICT 346 346 E -> R (IN REF. 2 AND 3).
SQ SEQUENCE 352 AA; 39235 MW; ED31C5CA02B70B19 CRC64;
Query Match 72.3%; Score 14; DB 1; Length 352;
Best local similarity 60.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cv 1 GPCXXFXIRY 10
Db 238 GPCGLGPKRY 247


```

QY 1 GPCXXFYRY 10
DB 84 GPCLAFFIRW 93

RESULT 2
Q968S8 PRELIMINARY; PRT; 76 AA.
ID Q968S8
AC Q968S8;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Silk protease inhibitor 1 precursor.
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
CX NCBI_TaxID=7137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21175824; PubMed=11277929;
RA Nirmala X., Kodrik D., Zurovec M., Sehnal P.;
RT "Insect silk contains both a Kunitz-type and a unique Kazal-type
proteinase inhibitor.";
RL Eur. J. Biochem. 268:2064-2073(2001).
DR EMBL; AF292098; AAK40037.1;
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PD00759; BASICTPASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Signal.
FT SIGNAL 1 20 POTENTIAL.
SQ SEQUENCE 76 AA; 8419 MW; 0C6ED5250632B79 CRC64;

Query Match 76.6%; Score 36; DB 5; Length 76;
Best Local Similarity 60.0%; Pred. No. 0.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXFYRY 10
DB 32 GPCRAAFORY 41

RESULT 3
Q95S22 PRELIMINARY; PRT; 461 AA.
ID Q95S22
AC Q95S22;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE HU01082p (CG6953-PB).
GN FAT-SPONDIN OR CG6953.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RP [2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Bianknoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brostier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

```

[6]

SEQUENCE FROM N.A.
FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY060990; AAL2838.1; -
EMBL; AE003804; AAM68494.1; -
FlyBase; FBGN0026721; fat-spondin.
GO; GO:0004867; F-serine protease inhibitor activity; IEA.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
Pfam; PF00014; Kunitz_BPTI; 1.
Pfam; PF00090; tsp; 1; 4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000223; Kunitz_BPTI; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS02079; BPTI_KUNITZ_2; 1.
PROSITE; PS50092; TSPI; 4.
Protease inhibitor; Serine protease inhibitor.
SEQUENCE 461 AA; 51517 MW; B77D074F1DB681B1 CRC64;

Query Match 76.6%; Score 36; DB 5; Length 461;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 GPCXXXPIRY 10
||| :||
349 GPCRGTYMRY 358

ILT 4
ZDO OSXZDO PRELIMINARY; PRT; 763 AA.
QXZDO;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Fat-spondin protein.
FAT-SPONDIN OR CG6953.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jallali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
PC Darocha S., Baumgartner S.;
RA "Fat-Spondin, a Drosophila member of the Spondin family, is highly
RT expressed in fat body and hemocytes.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003804; AAF57910.1; -
DR EMBL; AF135119; AAD31715.1; -
DR HSSP; P00974; IBTI.
DR FlyBase; FBGN0026721; fat-spondin.
DR GO; GO:0004867; F-serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002861; Reeler.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF02014; Reeler; 1.
DR Pfam; PF00090; tsp; 1; 4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000223; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00209; TSPI; 4.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50092; TSPI; 4.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 763 AA; 84945 MW; 3292DEDD2CFE4DAB CRC64;

Query Match 76.6%; Score 36; DB 5; Length 763;
Best Local Similarity 50.0%; Pred. No. 7;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPCXXXPIRY 10
||| :||
Db 651 GPCRGTYMRY 660

RESULT 5
ID QST7L9 PRELIMINARY; PRT; 76 AA.
AC QST7L9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kazal-type serine proteinase inhibitor 1.
GN SPI1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
CX NCBI_TaxID=7091;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21873253; PubMed=11881808;
RX Nirmala X., Mita K., Vanisree V., Zurovec M., Sehna F.;
RT "Identification of four small molecular mass proteins in the silk of
RT Bombyx mori.";
RT Insect Mol. Biol. 10:437-445(2001).
DR EMBL; AF352583; AAL83944.1; -
DR GO; GO:0004867; F-serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PR000222; Kunitz_BPTI; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS02079; BPTI_KUNITZ_1; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 76 AA; 8445 MW; AA3F97D373535A3B CRC64;

Query Match 74.5%; Score 35; DB 5; Length 76;
 Best Local Similarity 60.0%; Pred. No. 1.4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 4;

QY 1 GPCXXXFYRY 10
 ||| |||
 DB 32 GPCXGSPRY 41

RESULT 6

Q825I3 PRELIMINARY; PRT; 324 AA.
 AC Q825I3
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative reductase RfbI.
 GN RFB1 OR STY2303 OR T0779.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skellon J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18."
 RL J. Bacteriol. 185:2330-2337(2003).
 DR EMBL; ALG27273; CAD02456.1; -;
 DR EMBL; AE016836; AA068470.3; -;
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006058; 2Fe2S fd BS.
 DR InterPro; IPR008333; FAD_binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FPN cyt redctse.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR InterPro; IPR001221; Phe hydroxylase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDXLASE.
 DR PROSITE; PS00197; 2Fe2S FERREDOXIN; 1.
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 324 AA; 35884 MW; E3A556150F5CE199 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 324;
 Best Local Similarity 66.7%; Pred. No. 5.4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 3;

QY 1 GPCXXXFYR 9
 ||| |||
 DB 184 GPCGTFPR 192

RESULT 7

Q19315 PRELIMINARY; PRT; 580 AA.
 AC Q19315
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE F10F2.8 protein.
 GN F10F2.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coles L.;
 RV [2]
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99089613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z35598; CAA84654.1; -;
 DR PIR; T20716; T20716.
 DR WormPep; F10F2.8; CE00953.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
 SQ SEQUENCE 580 AA; 66437 MW; 08687AC6C55A7PDF CRC64;

Query Match 74.5%; Score 35; DB 5; Length 580;
 Best Local Similarity 50.0%; Pred. No. 9.2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3;

QY 1 GPCXXXFYRY 10
 ||| |||
 DB 395 GPCPAGFLQY 404

RESULT 8

Q45681 PRELIMINARY; PRT; 2225 AA.
 AC Q45681
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE W01F3.3 protein.
 GN W01F3.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cummings P.N.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

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MEDLINE-99069613; PubMed-9851916;
none;
"Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
Science 282:2012-2018(1998).
EMBL: Z92815; CAB07294.1; -.
PIR: T26063; T26063.
HSSP: P31713; ISHP.
WormPep; W01F3.3; CE16531.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000716; Thyroglobulin_1.
InterPro; IPR006150; Worm_repeat_1.
Pfam; PF00014; Kunitz_BPTI; 10.
Pfam; PF00086; thyroglobulin_1; 1.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000223; Kunitz_BPTI; 10.
SMART; SM00131; KU; 10.
SMART; SM00211; TY; 1.
SMART; SM00289; WRI; 4.
PROSITE; PS00280; BPTI_KUNITZ_1; 8.
PROSITE; PS00279; BPTI_KUNITZ_2; 10.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
Protease inhibitor; Serine protease inhibitor.
SEQUENCE 2225 AA; 242198 MW; ASDP8AE9D2A7B02A CRC64;

Query Match 74.5%; Score 35; DB 5; Length 2225;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFYRY 10
|||||
470 GPCGHSFYRY 479

ILT 9
174 O19474 PRELIMINARY; PRT; 91 AA.
O19474;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class I c5/g1L (Tla) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE-85206117; PubMed=3997208;
Rogers J.H.;
"Family organization of mouse H-2 class I genes.";
Immunogenetics 21:343-353(1985).
EMBL: M14828; AAA39688.1; -.
PIR: I68704; I68704.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
NON_TER 1
SEQUENCE 91 AA; 10671 MW; 4A5571396359805F CRC64;

Query Match 72.3%; Score 34; DB 7; Length 91;
Best Local Similarity 50.0%; Pred. No. 2.8;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 GPCXXXFYRY 10
|||||
71 GPCCKSLRY 80

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RESULT 10
Q8NAK6 PRELIMINARY; PRT; 224 AA.
ID Q8NAK6;
AC Q8NAK6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ35180.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092499; BAC03906.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR008296; TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
DR PIRSF; PIRSF001620; TFPI; 1.
DR KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 224 AA; 25795 MW; F586328C31344765 CRC64;

Query Match 72.3%; Score 34; DB 4; Length 224;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPCXXXFYRY 10
|||||
DB 32 GPCRALRY 41

Q62323 PRELIMINARY; PRT; 253 AA.
ID Q62323;
AC Q62323;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TL antigen (Fragment).
GN H2-T18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE-86010114; PubMed=3840195;
RX Chen Y.T., Obata Y., Stockert E., Old L.J.;
RT "Thymus-leukemia (TL) antigens of the mouse.";
J. Exp. Med. 162:1134-1148(1985).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; X03052; CAA26860.1; -.
DR PIR; I48850; I48850.
DR HSSP; P01901; IBOH.
DR MGD; MGI:95950; H2-T18.

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DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0006955; P: immune response; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 253 AA; 28532 MW; 5D0012815EC77FB1 CRC64;

Query Match 72.3%; Score 34; DB 11; Length 253;
 Best Local Similarity 50.0%; Pred. No. 7.3;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
 |||||
 Db 57 GPCCKDSLRY 66

RESULT 12

Q860A4
 ID Q860A4 PRELIMINARY; PRT; 272 AA.
 AC Q860A4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN MUCATL.
 OS Mus caroli (Wild mouse) (Ricefield mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10089;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tail;
 RX MEDLINE=22359207; PubMed=12471122;
 RA Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 RT "Hyperconservation of the putative antigen recognition site of the MHC
 class I-b molecule TL in the subfamily Murinae: evidence that thymus
 leukemia antigen is an ancient mammalian gene.";
 RL J. Immunol. 169:6890-6899(2002).
 DR EMBL; AY144137; AAP23911.1; -
 DR EMBL; AY144136; AAP23911.1; JOINED.
 DR GO; GO:0006955; P: immune response; IEA.
 DR GO; GO:0016020; C: membrane; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1
 SQ SEQUENCE 272 AA; 31647 MW; DF1FFBAFDFCB59 CRC64;

Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
 |||||
 Db 57 GPCCKDSLRY 66

Db 160 GPCCKDSLRY 169

RESULT 13

Q860A1
 ID Q860A1 PRELIMINARY; PRT; 272 AA.
 AC Q860A1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN MUABTL.
 OS Mus abbotti (Abbott's mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wild; TISSUE=Tail;
 RX MEDLINE=22359207; PubMed=12471122;
 RA Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
 RT "Hyperconservation of the putative antigen recognition site of the MHC
 class I-b molecule TL in the subfamily Murinae: evidence that thymus
 leukemia antigen is an ancient mammalian gene.";
 RL J. Immunol. 169:6890-6899(2002).
 DR EMBL; AY144133; AAP23909.1; -
 DR EMBL; AY144132; AAP23909.1; JOINED.
 DR GO; GO:0016020; C: membrane; IEA.
 DR GO; GO:0005489; P: electron transporter activity; IEA.
 DR GO; GO:0006118; P: electron transport; IEA.
 DR GO; GO:0006955; P: immune response; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON_TER 1
 SQ SEQUENCE 272 AA; 31380 MW; C8E5D1FD7028AB1A CRC64;

Query Match 72.3%; Score 34; DB 7; Length 272;
 Best Local Similarity 50.0%; Pred. No. 7.8;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPCXXXFYRY 10
 |||||
 Db 160 GPCCKDSLRY 169

RESULT 14

Q85Z29
 ID Q85Z29 PRELIMINARY; PRT; 272 AA.
 AC Q85Z29;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN MUCATL.
 OS Mus caroli (Wild mouse) (Ricefield mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10089;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tail;

MEDLINE=22359207; PubMed=12471122;
Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
"Hyperconservation of the putative antigen recognition site of the MHC
class I-b molecule TL in the subfamily Murinae: evidence that thymus
leukemia antigen is an ancient mammalian gene.";
J. Immunol. 169:6890-6899(2002).
EMBL; AY144139; AAP23912.1; JOINED.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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NON_TER 1
SEQUENCE 272 AA; 31592 MW; 2FBIFFBFCFDD5914 CRC64;
Query Match 72.3%; Score 34; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 GPCXXXFYRY 10
160 GPCKDSLRY 169
Q85ZZ6 PRELIMINARY; PRT; 272 AA.
Q85ZZ6;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (fragment).
MUDUTL.
Mus dunni (Pygmy mouse) (Mus terricolor).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10110;
[1]
SEQUENCE FROM N.A.
STRAIN=wild; TISSUE=Tail;
MEDLINE=22359207; PubMed=12471122;
Davis B.K., Cook R.G., Rich R.R., Rodgers J.R.;
"Hyperconservation of the putative antigen recognition site of the MHC
class I-b molecule TL in the subfamily Murinae: evidence that thymus
leukemia antigen is an ancient mammalian gene.";
J. Immunol. 169:6890-6899(2002).
EMBL; AY144145; AAP23915.1; JOINED.
EMBL; AY144144; AAP23915.1; JOINED.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000345; CytC heme-BS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 272 272
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Query Match 72.3%; Score 34; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 GPCXXXFYRY 10
160 GPCKDSLRY 169

Search completed: August 11, 2004, 13:09:24
Job time : 32.9048 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: August 11, 2004, 13:00:42 ; Search time 50.2857 Seconds
(without alignments)
61.807 Million cell updates/sec

le: US-10-661-207-2

fect score: 50

ence: 1 XGCXIVXPVC 11

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

imum DB seq length: 2000000000

:-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ibase :

A Geneseqp29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| alt no. | Score | Query Match | Length | DB ID | Description |
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| 1 | 44 | 88.0 | 50 | 1 AAP90597 | Aap90597 Sequence |
| 2 | 44 | 88.0 | 55 | 1 AAP90596 | Aap90596 Sequence |
| 3 | 44 | 88.0 | 55 | 1 AAP90595 | Aap90595 Sequence |
| 4 | 44 | 88.0 | 56 | 1 AAP82648 | Aap82648 Pancreat |
| 5 | 44 | 88.0 | 56 | 1 AAP82613 | Aap82613 Pancreat |
| 6 | 44 | 88.0 | 56 | 1 AAP82650 | Aap82650 Pancreat |
| 7 | 44 | 88.0 | 56 | 1 AAP82649 | Aap82649 Pancreat |
| 8 | 44 | 88.0 | 56 | 1 AAP82653 | Aap82653 Pancreat |
| 9 | 44 | 88.0 | 56 | 1 AAP82611 | Aap82611 Pancreat |
| 10 | 44 | 88.0 | 56 | 1 AAP82618 | Aap82618 Pancreat |
| 11 | 44 | 88.0 | 56 | 1 AAP82652 | Aap82652 Pancreat |
| 12 | 44 | 88.0 | 56 | 1 AAP82651 | Aap82651 Pancreat |
| 13 | 44 | 88.0 | 56 | 1 AAP82612 | Aap82612 Pancreat |
| 14 | 44 | 88.0 | 56 | 1 AAP82623 | Aap82623 Pancreat |
| 15 | 44 | 88.0 | 56 | 1 AAP80003 | Aap80003 Pancreat |
| 16 | 44 | 88.0 | 56 | 1 AAP90594 | Aap90594 Sequence |
| 17 | 44 | 88.0 | 56 | 2 AAR14631 | Aar14631 Pancreas |
| 18 | 44 | 88.0 | 56 | 2 AAR14632 | Aar14632 Pancreas |
| 19 | 44 | 88.0 | 56 | 2 AAR22622 | Aar22622 PTISI enco |
| 20 | 44 | 88.0 | 56 | 2 AAR65477 | Aar65477 Pancreat |
| 21 | 44 | 88.0 | 57 | 1 AAP81182 | Aap81182 Human pan |
| 22 | 44 | 88.0 | 57 | 1 AAP94152 | Aap94152 Sequence |
| 23 | 44 | 88.0 | 57 | 2 AAR03728 | Aar03728 Modified |
| 24 | 44 | 88.0 | 57 | 2 AAR03727 | Aar03727 Modified |
| 25 | 44 | 88.0 | 57 | 2 AAR14629 | Aar14629 Pancreas |

Aaw26361 Human pan
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Aar14630 Pancreas
Aap80400 Human pan
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Aar65482 Fusion pr
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Abg27312 Novel hum
Aar92296 PDKAN8 pr
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Abp57291 Kazal typ
Aar43918 Mutant mo
Aar43917 Mutant mo
Aar52229 Monitor p
Abp57286 Kazal typ
Abp57287 Kazal typ
Aap82622 Pancreati

ALIGNMENTS

RESULT 1

AAP90597
ID AAP90597 standard; protein; 50 AA.

XX AC AAP90597;

XX AC

XX 25-MAR-2003 (revised)

DT 11-JUN-1989 (first entry)

XX AC

DE Sequence of human pancreatic secretory trypsin inhibitor (PSTI).

XX KW

XX Human pancreatic secretory trypsin inhibitor; PSTI.

XX OS Homo sapiens.

XX FN EP300459-A.

XX PD 25-JAN-1989.

XX PF

XX 20-JUL-1988; 88EP-00111704.

XX PR

XX 23-JUL-1987; 87JP-00184556.

XX PA

XX (MOCH) MOCHIDA PHARM CO LTD.

XX (MORP) MORISHITA PHARM CO LTD.

XX PI Nobuhara M, Kanamori T, Ogino H, Mochida E;

XX XX

XX WPI; 1989-025643/04.

XX DR

XX Human pancreatic secretory trypsin inhibitor - obt'd. by recombinant DNA

XX PT techniques and free from other proteins of human origin.

XX PS

XX Claim 20; Page 20; 30pp; English.

XX SS

XX This sequence is produced by recombinant DNA techniques. A DNA sequence

XX encoding this is inserted into a vector alongside promoter, SD and signal

XX sequences and E.coli cells (pref. cell wall lipoprotein-deleted mutant

XX strains) transformed. The resulting product is free of any human protein

XX contaminants. It may be used in monoclonal antibody production and in

XX diagnosis of human pancreatic secretory inhibitor (PSTI)-related diseases

XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ

XX Sequence 50 AA;

XX Query Match 88.0%; Score 44; DB 1; Length 50;

XX Best Local Similarity 70.0%; Pred. NO. 0.57;

XX Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
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 Db 10 GCTKIYDPVC 19

RESULT 2
 AAP90596
 ID AAP90596 standard; protein; 55 AA.
 XX AC AAP90596;
 DT 25-MAR-2003 (revised)
 DT 11-JUN-1989 (first entry)
 XX DE Sequence of human pancreatic secretory trypsin inhibitor (PSTI).
 XX KW Human pancreatic secretory trypsin inhibitor; PSTI.
 XX OS Homo sapiens.
 XX PN EP300459-A.
 XX PD 25-JAN-1989.
 XX PF 20-JUL-1988; 88EP-00111704.
 XX PR 23-JUL-1987; 87JP-00184556.
 XX PA (MOCH) MOCHIDA PHARM CO LTD.
 XX PA (MORP) MORISHITA PHARM CO LTD.
 XX PI Nobuhara M, Kanamori T, Ogino H, Mochida E;
 XX WPI; 1989-025643/04.
 XX DR Human pancreatic secretory trypsin inhibitor - obt'd. by recombinant DNA
 XX PT techniques and free from other proteins of human origin.
 XX PS Claim 20; Page 20; 30pp; English.
 XX SQ Sequence 55 AA;
 Query Match 88.0%; Score 44; DB 1; Length 55;
 Best Local Similarity 70.0%; Pred. No. 0.62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GCXXIYXPVC 11
 |||||
 Db 15 GCTKIYDPVC 24

RESULT 3
 AAP90595
 ID AAP90595 standard; protein; 55 AA.
 XX AC AAP90595;
 XX DT 25-MAR-2003 (revised)
 DT 11-JUN-1989 (first entry)
 XX DE Sequence of human pancreatic secretory trypsin inhibitor (PSTI).
 XX KW Human pancreatic secretory trypsin inhibitor; PSTI.
 XX PI Nobuhara M, Kanamori T, Ogino H, Mochida E;
 XX WPI; 1989-025643/04.
 XX DR Human pancreatic secretory trypsin inhibitor - obt'd. by recombinant DNA
 XX PT techniques and free from other proteins of human origin.
 XX PS Claim 20; Page 20; 30pp; English.
 XX SQ Sequence 55 AA;
 Query Match 88.0%; Score 44; DB 1; Length 55;
 Best Local Similarity 70.0%; Pred. No. 0.62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GCXXIYXPVC 11
 |||||
 Db 15 GCTKIYDPVC 24

RESULT 4
 AAP82648
 ID AAP82648 standard; protein; 56 AA.
 XX AC AAP82648;
 XX DT 25-MAR-2003 (revised)
 DT 06-NOV-1990 (first entry)
 XX DE Pancreatic secretory trypsin inhibitor, PSTI 18 (Ile18).
 XX KW PSTI 18; pancreatic secretory trypsin inhibitor; protease;
 XX KW leukocyte elastase.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc-difference 18 /label= site-directed mutn.
 FT /note= "Lys>Ile"
 XX GB2199582-A.
 XX PD 13-JUL-1988.
 XX PF 07-JAN-1987; 87GB-00000204.
 XX PR 07-JAN-1987; 87GB-00000204.
 XX PA (FARB) BAYER AG.
 XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

OS Homo sapiens.
 XX PN EP300459-A.
 XX PD 25-JAN-1989.
 XX PF 20-JUL-1988; 88EP-00111704.
 XX PR 23-JUL-1987; 87JP-00184556.
 XX PA (MOCH) MOCHIDA PHARM CO LTD.
 XX PA (MORP) MORISHITA PHARM CO LTD.
 XX PI Nobuhara M, Kanamori T, Ogino H, Mochida E;
 XX WPI; 1989-025643/04.
 XX DR Human pancreatic secretory trypsin inhibitor - obt'd. by recombinant DNA
 XX PT techniques and free from other proteins of human origin.
 XX PS Claim 20; Page 20; 30pp; English.
 XX SQ Sequence 55 AA;
 Query Match 88.0%; Score 44; DB 1; Length 55;
 Best Local Similarity 70.0%; Pred. No. 0.62;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GCXXIYXPVC 11
 |||||
 Db 15 GCTKIYDPVC 24

RESULT 4
 AAP82648
 ID AAP82648 standard; protein; 56 AA.
 XX AC AAP82648;
 XX DT 25-MAR-2003 (revised)
 DT 06-NOV-1990 (first entry)
 XX DE Pancreatic secretory trypsin inhibitor, PSTI 18 (Ile18).
 XX KW PSTI 18; pancreatic secretory trypsin inhibitor; protease;
 XX KW leukocyte elastase.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc-difference 18 /label= site-directed mutn.
 FT /note= "Lys>Ile"
 XX GB2199582-A.
 XX PD 13-JUL-1988.
 XX PF 07-JAN-1987; 87GB-00000204.
 XX PR 07-JAN-1987; 87GB-00000204.
 XX PA (FARB) BAYER AG.
 XX PI Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

WPI; 1988-192315/28.
N-PSDB; AAN82228.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82649-54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 GCXXIYXPVC 11
||| ||| |||
15 GCTIYIRPVC 24

PI.T 5
32613

AAP82613 standard; protein; 56 AA.

AAP82613;

25-MAR-2003 (revised)
06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 3 (Tyr19, Glu19, Arg21).

PSTI 3; pancreatic secretory trypsin inhibitor; protease;
leukocyte elastase.

Synthetic.

Key Location/Qualifiers
Misc-difference 18 /label= site-directed mutn.
/note= "Lys>Tyr"
Misc-difference 19 /label= site-directed mutn.
/note= "Ile>Glu"
Misc-difference 21 /label= site-directed mutn.
/note= "Asn>Arg"

GB2199582-A.

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

WPI; 1988-192315/28.
N-PSDB; AAN82218.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

XX The protein was produced from a DNA sequence constructed from 25
CC oligonucleotides and is one of 24 analogues of PSTI. A master gene,
CC encoding PSTI 0, (having essentially the same sequence as reported by
CC L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template
CC for the construction of novel genes. See also AAP82611-23 and AAP82648-
CC 54. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ

Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPVC 11
||| ||| |||
Db 15 GCTIYIRPVC 24

RESULT 6

AAP82650

ID AAP82650 standard; protein; 56 AA.

XX AAP82650;

AC

XX 25-MAR-2003 (revised)

DT 06-NOV-1990 (first entry)

XX Pancreatic secretory trypsin inhibitor, PSTI 20 (Ile18, Asp21, Asn29).

XX PSTI 20; pancreatic secretory trypsin inhibitor; protease;
XX leukocyte elastase.

XX Synthetic.

Key Location/Qualifiers
FT Misc-difference 18 /label= site-directed mutn.
/note= "Lys>Val"
FT Misc-difference 21 /label= site-directed mutn.
/note= "Asn>Asp"
FT Misc-difference 29 /label= site-directed mutn.
/note= "Asp>Asn"

GB2199582-A.

13-JUL-1988.

XX 07-JAN-1987; 87GB-00000204.

XX 07-JAN-1987; 87GB-00000204.

XX (FARB) BAYER AG.

XX Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX WPI; 1988-192315/28.

XX N-PSDB; AAN82230.

XX Analogues of pancreatic secretory trypsin inhibitor - are protease
FT inhibitors with high specificity for leukocyte elastase.
XX
XX Claim 8; Page 62; 74pp; English.

XX The protein was produced from a DNA sequence constructed from 25
CC oligonucleotides and is one of 24 analogues of PSTI. A master gene,
CC encoding PSTI 0, (having essentially the same sequence as reported by
CC L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template
CC for the construction of novel genes. See also AAP82611-23 and AAP82648-
CC 54. (Updated on 25-MAR-2003 to correct PI field.)
XX

leukocyte elastase.

Synthetic.

Key Location/Qualifiers

Misc-difference 18
/label= site-directed mutn.
/note= "Lys>Leu"

GB2199582-A.

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

WPI; 1988-192315/28.

N-PSDB; AAN82216.

Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82612-23 and AAP82648-54

Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 GCXXIYXPVC 11

15 GCTLIYRPVC 24

JLT 10

32618

AAP82618 standard; protein; 56 AA.

AAP82618;

25-MAR-2003 (revised)

06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 7 (Leu19,Arg21).

PSTI 7; pancreatic secretory trypsin inhibitor; protease;
leukocyte elastase.

Synthetic.

Key Location/Qualifiers

Misc-difference 18
/label= site-directed mutn.
/note= "Lys>Leu"

Misc-difference 21
/label= site-directed mutn.
/note= "Asn>Arg"

GB2199582-A.

13-JUL-1988.

XX 07-JAN-1987; 87GB-00000204.

XX 07-JAN-1987; 87GB-00000204.

XX (FARB) BAYER AG.

XX Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX WPI; 1988-192315/28.

XX N-PSDB; AAN82222.

XX Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

XX Claim 8; Page 62; 74pp; English.

XX The protein was produced from a DNA sequence constructed from 25 oligonucleotides and is one of 24 analogues of PSTI. A master gene, encoding PSTI 0, (having essentially the same sequence as reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template for the construction of novel genes. See also AAP82611-23 and AAP82648-54. (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;

Best Local Similarity 70.0%; Pred. No. 0.63;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11

15 GCTLIYRPVC 24

RESULT 11

AAP82652

ID AAP82652 standard; protein; 56 AA.

XX AC AAP82652;

XX 25-MAR-2003 (revised)

DT 06-NOV-1990 (first entry)

DE Pancreatic secretory trypsin inhibitor, PSTI 22 (Tyr18).

KW PSTI 22; pancreatic secretory trypsin inhibitor; protease;

KW leukocyte elastase.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 18

FT /label= site-directed mutn.

FT /note= "Lys>Tyr"

XX GB2199582-A.

PN 13-JUL-1988.

XX 07-JAN-1987; 87GB-00000204.

XX 07-JAN-1987; 87GB-00000204.

XX (FARB) BAYER AG.

XX Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX WPI; 1988-192315/28.

XX N-PSDB; AAN82232.

XX Analogues of pancreatic secretory trypsin inhibitor - are protease inhibitors with high specificity for leukocyte elastase.

PT

2 GCXXIYXPVC 11
|||
15 GCTLIYDPVC 24

HLT 14

2623
AAP82623 standard; protein; 56 AA.

AAP82623;

25-MAR-2003 (revised)
06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 17 (Val18).

PSTI 17; pancreatic secretory trypsin inhibitor; protease;
leukocyte elastase.

Synthetic.

Key Location/Qualifiers
Misc-difference 18 /label= site-directed mutn.
/note= "Iys>Val"

GB2199582-A.

13-JUL-1988.

07-JAN-1987; 87GB-00000204.

07-JAN-1987; 87GB-00000204.

(FARB) BAYER AG.

Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

WPI; 1988-192315/28.

N-PSDB; AAN82227.

Analogues of pancreatic secretory trypsin inhibitor - are protease
inhibitors with high specificity for leukocyte elastase.

Claim 8; Page 62; 74pp; English.

The protein was produced from a DNA sequence constructed from 25
oligonucleotides and is one of 24 analogues of PSTI. A master gene,
encoding PSTI 0, (having essentially the same sequence as reported by
L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as a template
for the construction of novel genes. See also AAP82611-22 and AAP82648-
54. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 GCXXIYXPVC 11
|||
15 GCTVIYNPVC 24

HLT 15

10003

AAP80003 standard; protein; 56 AA.

AAP80003;

06-NOV-1990 (first entry)

Pancreatic secretory trypsin inhibitor, PSTI 0.

XX PSTI 0; pancreatic secretory trypsin inhibitor; protease;
KW leukocyte elastase.

XX Synthetic.

XX GB2199582-A.

XX 13-JUL-1988.

XX 07-JAN-1987; 87GB-00000204.

XX 07-JAN-1987; 87GB-00000204.

XX (FARB) BAYER AG.

XX Collins D, Blocker H, Frank R, Maywald F, Fritz H, Bruns W;

XX WPI; 1988-192315/28.

XX N-PSDB; AAN80030.

XX Analogues of pancreatic secretory trypsin inhibitor - are protease
inhibitors with high specificity for leukocyte elastase.

XX Disclosure; Page 7; 74pp; English.

XX The protein was produced from a DNA sequence constructed from 25
oligonucleotides and has the same sequence as the natural PSTI 0. A
master gene, encoding PSTI 0, (having essentially the same sequence as
reported by L.J. Greene, 1976, Methods Enzymol. 45, 813-825) was used as
a template for the construction of novel genes. See also AAP82611-23 and
AAP82648-54

XX Sequence 56 AA;

Query Match 88.0%; Score 44; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GCXXIYXPVC 11

Db 15 GCTVIYNPVC 24

Search completed: August 11, 2004, 13:07:40
Job time : 51.2857 secs

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>protein - protein search, using sw model

on: August 11, 2004, 13:04:58 ; Search time 12.0476 Seconds
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87.827 Million cell updates/sec

le: US-10-661-207-2

ect score: 50

ence: 1 XGCXXIYXPC 11

ing table: BLOSUM62

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al number of hits satisfying chosen parameters: 283366

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imum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

ibase :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Alt No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 44 | 88.0 | 79 | TIHUA | pancreatic secreto |
| 2 | 42 | 84.0 | 56 | TIHUA | pancreatic secreto |
| 3 | 42 | 84.0 | 56 | TIHUA | pancreatic secreto |
| 4 | 42 | 84.0 | 56 | TIHUA | pancreatic secreto |
| 5 | 42 | 84.0 | 57 | TIHUA | pancreatic secreto |
| 6 | 42 | 84.0 | 79 | TIHUA | pancreatic secreto |
| 7 | 42 | 84.0 | 80 | TIHUA | pancreatic secreto |
| 8 | 38 | 76.0 | 86 | TIHUA | peptide PEC-60 pre |
| 9 | 38 | 76.0 | 472 | TIHUA | ovoinhibitor precu |
| 10 | 38 | 76.0 | 1959 | TIHUA | agrin - rat |
| 11 | 37 | 74.0 | 53 | TIHUA | ovomucoid, third d |
| 12 | 36 | 72.0 | 1699 | TIHUA | voltage-gated sodi |
| 13 | 35 | 70.0 | 79 | TIHUA | pancreatic secreto |
| 14 | 35 | 70.0 | 93 | TIHUA | hypothetical lik p |
| 15 | 35 | 70.0 | 1154 | TIHUA | diacylglycerol kin |
| 16 | 34 | 68.0 | 94 | TIHUA | nucleic acid-bind |
| 17 | 34 | 68.0 | 341 | TIHUA | ecdysone-inducible |
| 18 | 34 | 68.0 | 746 | TIHUA | hypothetical prote |
| 19 | 33 | 66.0 | 54 | TIHUA | ovomucoid, third d |
| 20 | 33 | 66.0 | 772 | TIHUA | hypothetical prote |
| 21 | 33 | 66.0 | 802 | TIHUA | hypothetical prote |
| 22 | 33 | 66.0 | 2422 | TIHUA | fatty-acid synthas |
| 23 | 32 | 64.0 | 128 | TIHUA | hypothetical prote |
| 24 | 32 | 64.0 | 201 | TIHUA | receptor like prot |
| 25 | 32 | 64.0 | 201 | TIHUA | receptor like prot |
| 26 | 32 | 64.0 | 223 | TIHUA | thymidine kinase U |
| 27 | 32 | 64.0 | 572 | TIHUA | hypothetical prote |
| 28 | 32 | 64.0 | 609 | TIHUA | hypothetical prote |
| 29 | 32 | 64.0 | 727 | TIHUA | FA0F12.5 protein - |

RESULT 1

TIHUA

pancreatic secretory trypsin inhibitor precursor [validated] - human

N;Alternate names: endothelial cell growth factor 2a

C;Species: Homo sapiens (man)

C;Date: 30-Nov-1980 #sequence, revision 17-Feb-1994 #text, change 08-Dec-2000

C;Accession: A27484; S02605; A90062; A92355; A25604; I52210; A01229

R;Horii, A.; Kobayashi, T.; Tomita, N.; Yamamoto, T.; Fukushima, S.; Murotsu, T.; Ogawa, Biochem. Biophys. Res. Commun. 149, 635-641, 1987

A;Title: Primary structure of human pancreatic secretory trypsin inhibitor (PSTI) gene.

A;Reference number: A27484; MUID:88106485; PMID:3501289

A;Accession: A27484

A;Molecule type: DNA

A;Residues: 1-79 <HOR>

A;Cross-references: GB:M20510; GB:M18374; NID:9190692; PIDN:AAA36522.1; PID:9190694

R;Tomita, N.; Horii, A.; Yamamoto, T.; Ogawa, M.; Mori, T.; Matsubara, K. FEBS Lett. 225, 113-119, 1987

A;Title: Expression of pancreatic secretory trypsin inhibitor gene in neoplastic tissues

A;Reference number: S02605; MUID:88083571; PMID:2961612

A;Accession: S02605

A;Molecule type: mRNA

A;Residues: 1-63, 'G', 65-79 <TOM>

A;Cross-references: EMBL:Y00705; NID:935765; PIDN:CAN68697.1; PID:935766

A;Note: The authors translated the codon TAC for residue 33 as Thr and GGT for residue 64

R;Bartelt, D.C.; Shapanka, R.; Greene, L.J. Arch. Biochem. Biophys. 179, 189-199, 1977

A;Title: The primary structure of the human pancreatic secretory trypsin inhibitor. Amino

A;Reference number: A90062; MUID:77133145; PMID:843082

A;Accession: A90062

A;Molecule type: protein

A;Residues: 24-43, 'N', 45-51, 'D', 53-79 <BAR>

A;Note: the inhibitor is present in multiple chromatographic forms differing in asparagin

R;Huhtala, M.L.; Pesonen, K.; Kalkkinen, N.; Stenman, U.H. J. Biol. Chem. 257, 13713-13716, 1982

A;Title: Purification and characterization of a tumor-associated trypsin inhibitor from t

A;Reference number: A92355; MUID:83056875; PMID:7142173

A;Accession: A92355

A;Molecule type: protein

A;Residues: 24-31, 'X', 33-38, 'X', 40-43, 'N', 45-46 <HUH>

A;Note: this peptide was isolated from the urine of a patient with ovarian cancer

R;McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A. J. Biol. Chem. 261, 5378-5383, 1986

A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells are

A;Reference number: A92583; MUID:86168278; PMID:3007499

A;Accession: A25604

A;Molecule type: protein

A;Residues: 24-31, 'X', 33-38, 'X', 40-46, 'X', 48 <MCK>

R;Yamamoto, T.; Nakamura, Y.; Nishide, T.; Emi, M.; Ogawa, M.; Mori, T.; Matsubara, K. Biochem. Biophys. Res. Commun. 132, 605-612, 1985

A;Title: Molecular cloning and nucleotide sequence of human pancreatic secretory trypsin

A;Reference number: I52210; MUID:86050645; PMID:3877508

A;Accession: I52210

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-79 <RES>

C:Cross-references: GB:M11949; MID:g190687; PIDN:AAA36521.1; PID:g190688

C:Genetics:

A:Gene: GDB:SPINK1

A:Cross-references: GDB:120383; OMIM:167790

A:Map position: Sq31-5q33

A:Introns: 19/1; 29/3; 65/2

C:Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog

C:Keywords: monomer; pancreas; serine proteinase inhibitor

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-79/Product: pancreatic secretory trypsin inhibitor #status experimental <MAP>

F:30-79/Domain: Kazal proteinase inhibitor homolog <KPI>

F:32-61,39-58,47-79/Disulfide bonds: #status predicted

F:41/Inhibitory site: Lys (trypsin) #status predicted

Query Match 84.0%; Score 44; DB 1; Length 79;

Best Local Similarity 70.0%; Pred. No. 0.11;

Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 GCXXIYXPVC 11

Db 38 GCTKIYDPVC 47

RESULT 2

TIBOA

pancreatic secretory trypsin inhibitor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Jul-1999

C:Accession: A01230

R:Greene, L.J.; Bartelt, D.C.

J. Biol. Chem. 244, 2646-2657, 1969

A:Title: The structure of the bovine pancreatic secretory trypsin inhibitor - Kazal's in

A:Reference number: A92046; MUID:69187206; PMID:5769997

A:Accession: A01230

A:Molecule type: protein

A:Residues: 1-56 <GRE>

R:Guy, O.; Shepanka, R.; Greene, L.J.

J. Biol. Chem. 246, 7740-7747, 1971

A:Title: The structure of the bovine pancreatic secretory trypsin inhibitor-Kazal's inhi

A:Reference number: A92057; MUID:72086018; PMID:5135319

A:Contents: annotation; disulfide bonds

R:Rigbi, M.; Greene, L.J.

J. Biol. Chem. 243, 5457-5464, 1968

A:Title: Limited proteolysis of the bovine pancreatic secretory trypsin inhibitor at ac

A:Reference number: A92037; MUID:69080142; PMID:5750336

A:Contents: annotation; inhibitory site

C:Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog

C:Keywords: pancreas; serine proteinase inhibitor

F:7-56/Domain: Kazal proteinase inhibitor homolog <KPI>

F:9-38,16-35,24-56/Disulfide bonds: #status experimental

F:18/Inhibitory site: Arg (trypsin) #status experimental

Query Match 84.0%; Score 42; DB 1; Length 56;

Best Local Similarity 70.0%; Pred. No. 0.21;

Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 GCXXIYXPVC 11

Db 15 GCPRIYNPVC 24

RESULT 3

TISHA

pancreatic secretory trypsin inhibitor - sheep (tentative sequence)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

C:Accession: A94487; A01230

R:Tschesche, H.; Obermeier, R.; Hochstrasser, K.

unpublished results, cited by Tschesche, H., Wachter, E., Kupfer, S., Obermeier, R., Reif

Inhibitors, Fritz, H., and Tschesche, H., eds., pp.207-222, Walter de Gruyter, New York

A:Reference number: A94487

A:Accession: A94487

A:Molecule type: protein

A:Residues: 1-56 <TSC>

C:Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog

C:Keywords: pancreas; serine proteinase inhibitor

F:7-56/Domain: Kazal proteinase inhibitor homolog <KPI>

F:9-38,16-35,24-56/Disulfide bonds: #status predicted

F:18/Inhibitory site: Arg (trypsin) #status predicted

Query Match 84.0%; Score 42; DB 1; Length 56;

Best Local Similarity 70.0%; Pred. No. 0.21;

Matches 7; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GCXXIYXPVC 11

Db 15 GCPRIYNPVC 24

RESULT 4

TIPG

pancreatic secretory trypsin inhibitor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Jul-1999

C:Accession: A91174; A92079; A91647; A90646; A01231

R:Tschesche, H.; Wachter, E.

Eur. J. Biochem. 16, 187-198, 1970

A:Title: The structure of the porcine pancreatic secretory trypsin inhibitor I. A seq

A:Reference number: A91174; MUID:70283430; PMID:5466061

A:Contents: PSTI I

A:Accession: A91174

A:Molecule type: protein

A:Residues: 1-56 <TSI>

R:Bartelt, D.C.; Greene, L.J.

J. Biol. Chem. 246, 2218-2229, 1971

A:Title: The primary structure of the porcine pancreatic secretory trypsin inhibitor :

A:Reference number: A92079; MUID:71178430; PMID:5103069

A:Accession: A92079

A:Molecule type: protein

A:Residues: 1-56 <BAR>

R:Tschesche, H.; Schneider, M.; Reidel, G.; Klein, H.

Hoppe-Seyler's Z. Physiol. Chem. 353, 763-764, 1972

A:Title: Die Disulfidbrücken des sekretorischen Schweinepankreas-Trypsininhibitors u

A:Reference number: A91654; MUID:73001409; PMID:4672150

A:Contents: annotation; disulfide bonds

R:Tschesche, H.; Wachter, E.

Hoppe-Seyler's Z. Physiol. Chem. 351, 1449-1459, 1970

A:Title: Die Primärstruktur des spezifischen Trypsininhibitors II (Kazal-Typ) aus S

A:Reference number: A91647; MUID:71092915; PMID:5531651

A:Contents: PSTI II

A:Accession: A91647

A:Molecule type: protein

A:Residues: 5-56 <TS2>

R:Menegatti, E.; Bortolotti, F.; Minchiotti, L.; de Marco, A.

Biochim. Biophys. Acta 707, 50-58, 1982

A:Title: Isolation and characterization of a new form of the porcine pancreatic secret

A:Reference number: A90646; MUID:83049107; PMID:7138878

A:Contents: PSTI III

A:Accession: A90646

A:Molecule type: protein

A:Residues: 9-56 <MEN>

C:Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog

C:Keywords: pancreas; serine proteinase inhibitor

F:7-56/Domain: Kazal proteinase inhibitor homolog <KPI>

F:9-38,16-35,24-56/Disulfide bonds: #status experimental

F:18/Inhibitory site: Lys (trypsin) #status experimental

Query Match 84.0%; Score 42; DB 1; Length 56;

Best Local Similarity 70.0%; Pred. No. 0.21;

Matches 7; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GCXXIYXPVC 11

Db 15 GCPRIYNPVC 24

A;Title: Purification and characterization of a trypsin inhibitor from mouse seminal vesicle
A;Reference number: S18384; MUID:92027737; PMID:1929395
A;Accession: S18384
A;Molecule type: Protein
A;Residues: 43-47;49-58;60-61;63-72 <LA1>
C;Comment: The expression of this inhibitor is dependent upon testosterone in prostate. s
C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C;Keywords: pancreas; prostate; seminal vesicle; serine proteinase inhibitor; testis
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-80/Product: pancreatic secretory trypsin inhibitor #status predicted <MAT>
F;31-80/Domain: Kazal proteinase inhibitor homolog <KPI>
F;33-62,40-59,48-80/Dialufide bonds: #status predicted
F;42/Inhibitory site: Arg (trypsin) #status predicted
Query Match 84.0%; Score 42; DB 1; Length 80;
Best Local Similarity 70.0%; Pred. No. 0.26;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GCXIYXPVC 11
Db 39 GCPRIYDVC 48
||| ||| |||
RESULT 8
A3427
peptide PEC-60 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: A44041; A34427; S24956
R;Metis, M.; Cintra, A.; Solfrini, V.; Ernfor, P.; Bortolotti, F.; Morrasutti, D.G.; C
J. Biol. Chem. 267, 19823-19832, 1992
A;Title: Molecular cloning of PEC-60 and expression of its mRNA and peptide in the gastr
A;Reference number: A44041; MUID:93015834; PMID:1400298
A;Accession: A44041
A;Molecule type: mRNA
A;Residues: 1-86 <MET>
A;Cross-references: EMBL:X67109; NID:92033; PIDN:CAA47482.1; PID:G2034
A;Note: sequence extracted from NCBI Backbone (NCBIP:115615)
F;Agerberth, B.; Soederling-Barros, J.; Joernvall, H.; Chen, Z.; Oestenson, C.G.; Efend
Proc. Natl. Acad. Sci. U.S.A. 86, 8590-8594, 1989
A;Title: Isolation and characterization of a 60-residue intestinal peptide structurally
A;Reference number: A34427; MUID:90046843; PMID:2573065
A;Accession: A34427
A;Molecule type: protein
A;Residues: 27-86 <AGE>
C;Comment: This peptide does not inhibit trypsin. Its biological function is unknown, al
C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C;Keywords: intestine; leukocyte; serine proteinase inhibitor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-86/Product: peptide PEC-60 #status experimental <MAT>
F;35-86/Domain: Kazal proteinase inhibitor homolog <KPI>
F;37-68,46-65/Dialufide bonds: #status predicted
F;48/Inhibitory site: Arg (unidentified proteinase) #status predicted
F;54-86/Dialufide bonds: #status experimental
Query Match 76.0%; Score 38; DB 1; Length 85;
Best Local Similarity 66.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CXXIYXPVC 11
Db 46 CSRIYDVC 54
||| ||| |||
RESULT 9
A26730
ovoinhibitor precursor [validated] - chicken
N;Contains: serine proteinase inhibitor (Kazal type)
C;Species: Gallus gallus (chicken)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Sep-2000
C;Accession: A26730
R;Scott, M.J.; Huckaby, C.S.; Kato, I.; Kohr, W.J.; Laskowski Jr., M.; Tsai, M.J.; O'Ma

J. Biol. Chem. 262, 5899-5907, 1987
A;Title: Ovoinhibitor introns specify functional domains as in the related and linked
A;Reference number: A26730; MUID:87194792; PMID:3571241
A;Accession: A26730
A;Molecule type: mRNA; protein
A;Residues: 1-472 <SC0>
A;Cross-references: GB:M16141; NID:G212483; PIDN:AAA48994.1; PID:G212485
A;Note: parts of this sequence, including the amino end of the mature protein, were d
C;Comment: This is a major inhibitor in blood plasma and also occurs in egg white.
C;Superfamily: chicken ovoinhibitor; Kazal proteinase inhibitor homolog
C;Keywords: duplication; egg white; plasma; serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-472/Product: ovoinhibitor #status predicted <MAT>
F;26-85/Domain: Kazal proteinase inhibitor homolog <KPI1>
F;92-150/Domain: Kazal proteinase inhibitor homolog <KPI2>
F;157-216/Domain: Kazal proteinase inhibitor homolog <KPI3>
F;223-282/Domain: Kazal proteinase inhibitor homolog <KPI4>
F;289-347/Domain: Kazal proteinase inhibitor homolog <KPI5>
F;354-413/Domain: Kazal proteinase inhibitor homolog <KPI6>
F;420-472/Domain: Kazal proteinase inhibitor homolog <KPI7>
F;28-67,45-64,53-85,94-132,110-129,118-150,159-198,176-195,184-216,225-264,242-261,251
F;47/Inhibitory site: Arg (serine proteinase) #status predicted
F;112/Inhibitory site: Arg (serine proteinase) #status predicted
F;178/Inhibitory site: Arg (serine proteinase) #status predicted
F;244/Inhibitory site: Arg (serine proteinase) #status predicted
F;309/Inhibitory site: Phe (serine proteinase) #status predicted
F;375/Inhibitory site: Met (serine proteinase) #status predicted
F;434/Inhibitory site: Met (serine proteinase) #status predicted
Query Match 76.0%; Score 38; DB 1; Length 472;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CXXIYXPVC 11
Db 373 CTMIYDVC 381
||| ||| |||
RESULT 10
AGRT
agrin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 17-Nov-2000
C;Accession: JH0399; A38856
R;Rupp, F.; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
A;Accession: JH0399
A;Molecule type: mRNA
A;Residues: 1-1779;1799-1959 <RUP>
A;Cross-references: GB:M64780; NID:G202798; PIDN:AAA40703.1; PID:G202800
A;Experimental source: embryonic spinal cord
A;Note: it is uncertain whether Met-1, Met-18, or Met-24 is the initiator
R;Rupp, F.; Oezcelik, T.; Linial, M.; Peterson, K.; Francke, U.; Scheller, R.
J. Neurosci. 12, 3595-3544, 1992
A;Title: Structure and chromosomal localization of the mammalian agrin gene.
A;Reference number: A38856; MUID:92407628; PMID:1326608
A;Accession: A38856
A;Molecule type: mRNA
A;Residues: 1780-1798 <RU2>
A;Cross-references: GB:S44194
C;Comment: This protein mediates the motor neuron-induced aggregation of acetylcholin
C;Superfamily: agrin; EGF homolog; Kazal proteinase inhibitor homolog; laminin G re
C;Keywords: alternative splicing; duplication; agrin, form 1 #status predicted <AG1>
F;1-1959/Product: agrin, form 1 #status predicted <AG1>
F;1-1787,1799-1959/Product: agrin, form 4 #status predicted <AG4>
F;1-1779,1799-1959/Product: agrin, form 3 #status predicted <AG3>
F;1-1779,1788-1959/Product: agrin, form 5 #status predicted <AG5>
F;1-1143,1153-1959/Product: agrin, form 2 #status predicted <AG2>
F;22-50/Region: hydrophobic

1-137/Domain: Kazal proteinase inhibitor homology <KPI1>
3-212/Domain: Kazal proteinase inhibitor homology <KPI2>
6-284/Domain: Kazal proteinase inhibitor homology <KPI3>
7-356/Domain: Kazal proteinase inhibitor homology <KPI4>
1-429/Domain: Kazal proteinase inhibitor homology <KPI5>
6-494/Domain: Kazal proteinase inhibitor homology <KPI6>
1-559/Domain: Kazal proteinase inhibitor homology <KPI7>
0-542/Region: motor neuron attachment (L-R-E) motif
16-645/Domain: Kazal proteinase inhibitor homology <KPI8>
18-739/Domain: laminin-type EGF-like homology <LE1>
2-786/Domain: laminin-type EGF-like homology <LE2>
4-864/Domain: Kazal proteinase inhibitor homology <KPI9>
19-992/Region: serine/threonine-rich
184-1086/Region: motor neuron attachment (L-R-E) motif
47-1215/Region: serine/threonine-rich
224-1257/Domain: EGF homology <EG1>
287-1442/Domain: laminin G repeat homology <LG1>
144-1476/Domain: EGF homology <EG2>
183-1515/Domain: EGF homology <EG3>
155-1706/Domain: laminin G repeat homology <LG2>
113-1747/Domain: EGF homology <EG4>
107-1959/Domain: laminin G repeat homology <LG3>
17-116-105-137-171-191-180-212-244-263-252-284-316-335-324-356-389-408-397-429-454-473
16-1483-1494-1488-1504-1506-1515/Disulfide bonds: #status predicted
15-672-827-957/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.0%; Score 38; DB 1; Length 1959;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3 CXIYXPVC 11
| | | | |
389 CSGIYDPVC 397

TLT 11
138
nucoid, third domain - Coqui francolin (fragment)
Species: Francolinus coqui (Coqui francolin)
Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Feb-1997
Accession: G31438
skowski Jr., M.; Kato, I.; Ardel, W.; Cook, J.; Denton, A.; Empie, M.W.; Kohr, W.J.
.; Wicczorek, M.
Chemistry 26, 202-221, 1987
Title: Ovumucoid third domains from 100 avian species: isolation, sequences, and hyper
reference number: A90515; MUID:87157615; PMID:3828298
Accession: G31438
Molecule type: protein
Residues: 1-53 <LAS>
Note: the authors designate this sequence with the code OMCOF3
perfamily: ovomucoid; Kazal proteinase inhibitor homology
ywords: egg white; glycoprotein; serine proteinase inhibitor
-53/Domain: Kazal proteinase inhibitor homology <KPI>
-35,13-32,21-53/Disulfide bonds: #status predicted
5/Binding site: carbohydrate (Asn) (covalent) #status absent
2/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 74.0%; Score 37; DB 2; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 GCXXIYXPVC 11
| | | | |
12 GCTWEYRDPVC 21

UUT 12
340
rage-gated sodium channel homolog - Bdelloura candida
Species: Bdelloura candida
Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
Accession: T31340
ezioriski, M.C.; Greenberg, R.M.; Anderson, P.A.

submitted to the EMBL Data Library, March 1997
A;Description: A putative voltage-gated sodium channel from the turbellarian flatworm Bde
A;Reference number: Z21006
A;Accession: T31340
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-1699 <JEZ>
A;Cross-references: EMBL:U93074; NID:G1947093; PID:G1947094; PIDN:AAC63049.1
C;Genetics:
A;Gene: Nal
C;Superfamily: sodium channel protein

Query Match 72.0%; Score 36; DB 2; Length 1699;
Best Local Similarity 55.6%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CXIYXPVC 11
| | | | |
DB 469 CDDIYQPIC 477

RESULT 13
TIRT2
pancreatic secretory trypsin inhibitor II precursor - rat
N;Alternate names: hepatic proteinase inhibitor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: B3292; S28947; S00634; S08982
R;Horii, A.; Tomita, N.; Yokouchi, H.; Doi, S.; Uda, K.; Ogawa, M.; Mori, T.; Matsubara,
Biochem. Biophys. Res. Commun. 162, 151-159, 1989
A;Title: On the cDNA's for two types of rat pancreatic secretory trypsin inhibitor.
A;Reference number: A33292; MUID:89322336; PMID:2751646
A;Accession: B3292
A;Molecule type: mRNA
A;Residues: 1-79 <HOR>
A;Cross-references: GB:M27883
R;Tazuki, S.; Miura, Y.; Fushiki, T.; Oomori, T.; Satoh, T.; Natori, Y.; Sugimoto, E.
Biochim. Biophys. Acta 1132, 199-202, 1992
A;Title: Molecular cloning and characterization of genes encoding rat pancreatic cholecys
A;Reference number: S28946; MUID:93003324; PMID:1390891
A;Accession: S28947
A;Molecule type: DNA
A;Residues: 1-79 <TSU>
A;Cross-references: DDBJ:D11325; NID:Q220805; PIDN:BAA01945.1; PID:Q220887
R;Uda, K.; Ogawa, M.; Shibata, T.; Murata, A.; Mori, T.; Kikuchi, N.; Yoshida, N.; Tsur
Biol. Chem. Hoppe-Seyler 369(Suppl.), 53-61, 1988
A;Title: Purification, characterization and amino-acid sequencing of two pancreatic secr
A;Reference number: S00633; MUID:89076534; PMID:3202973
A;Accession: S00634
A;Molecule type: protein
A;Residues: 24-79 <UDA>
R;Kido, H.; Yokoguchi, Y.; Katunuma, N.
Eur. J. Biochem. 188, 501-506, 1990
A;Title: A low-molecular-mass Kazal-type protease inhibitor isolated from rat hepatocyte
A;Reference number: S08982; MUID:90235819; PMID:2110056
A;Accession: S08982
A;Molecule type: protein
A;Residues: 24-79 <KID>
C;Genetics:
A;Introns: 19/1; 29/3; 65/2
C;Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C;Keywords: pancreas; serine proteinase inhibitor
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-79/Product: pancreatic secretory trypsin inhibitor I #status experimental <MAT>
F;30-79/Domain: Kazal proteinase inhibitor homology <KPI>
F;32-61,39-58,47-79/Disulfide bonds: #status predicted
F;41/Inhibitory site: Arg (trypsin) #status predicted

Query Match 70.0%; Score 35; DB 1; Length 79;
Best Local Similarity 60.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCXXIYXPVC 11

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Db          38 GCFRDYDFVC 47
|| | | |
RESULT 14
JA0128
hypothetical 11K protein - potato virus S
C:Species: potato virus S
A:Note: host Chenopodium quinoa
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JA0128
J:MacKenzie, D.J.; Tremaine, J.H.; Stace-Smith, R.
R:Gen. Virol. 70, 1053-1063, 1989
A:Title: Organization and interl viral homologues of the 3'-terminal portion of potato virus
A:Reference number: JA0123; MUID:89279283; PMID:2732711
A:Accession: JA0128
A:Molecule type: Genomic RNA
A:Residues: 1-93 <MAC>
A:Cross-references: GB:D00461; MID:g222438; PIDN:BAA00356.1; PID:g2160373
C:Comment: The genome is a single-stranded, positive-sense RNA.
C:Superfamily: potato virus nucleic acid-binding protein
C:Keywords: DNA binding; zinc finger

Query Match          70.0%; Score 35; DB 2; Length 93;
Best Local Similarity 55.6%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXIYXPVC 11
| : | | |
Db 57 CYRVPPVC 65

RESULT 15
TI8525
diacylglycerol kinase (EC 2.7.1.107) eta - hamster
N:Alternate names: diglyceride kinase
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: TI8525
R:Klauck, T.M.; Xu, X.; Mousseau, B.; Jaken, S.
J: Biol. Chem. 271, 19781-19788, 1996
A:Title: Cloning and characterization of a glucocorticoid-induced diacylglycerol kinase.
A:Reference number: Z18948; MUID:96355275; PMID:8702685
A:Accession: TI8525
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1154 <KLA>
A:Cross-references: EMBL:U59429; NID:g1401231; PID:g1401232; PIDN:AAC52714.1
A:Experimental source: strain Syrian
C:Superfamily: protein kinase C zinc-binding repeat homology
C:Keywords: phosphotransferase
F:170-219/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match          70.0%; Score 35; DB 2; Length 1154;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXIYXPVC 11
| : | | |
Db 284 CKDLYHEVC 292

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Search completed: August 11, 2004, 13:09:59
 Job time : 13.0476 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: August 11, 2004, 13:01:12 ; Search time 8.38095 Seconds
(without alignments)
69.342 Million cell updates/sec

le: US-10-661-207-2

fect score: 50

lence: 1 XGCXXIYXPCV 11

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 141681 seqs, 52070155 residues

al number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

--processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ibase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| alt No. | Score | Query Match | Length | DB ID | Description |
|---------|-------|-------------|--------|-------|-------------|
| 1 | 44 | 88.0 | 56 | 1 | IPK1_HORSE |
| 2 | 44 | 88.0 | 79 | 1 | IPK1_HUMAN |
| 3 | 42 | 84.0 | 56 | 1 | IPK1_BOVIN |
| 4 | 42 | 84.0 | 56 | 1 | IPK1_PIG |
| 5 | 42 | 84.0 | 56 | 1 | IPK1_SHEEP |
| 6 | 42 | 84.0 | 57 | 1 | IPK1_CANFA |
| 7 | 42 | 84.0 | 79 | 1 | IPK1_RAT |
| 8 | 42 | 84.0 | 80 | 1 | ISK3_MOUSE |
| 9 | 40 | 80.0 | 69 | 1 | IPK1_STRCA |
| 10 | 39 | 78.0 | 197 | 1 | MCPI_MELCP |
| 11 | 38 | 76.0 | 86 | 1 | ISK4_PIG |
| 12 | 38 | 76.0 | 156 | 1 | ESM1_DROME |
| 13 | 38 | 76.0 | 472 | 1 | IOV7_CHICK |
| 14 | 38 | 76.0 | 1959 | 1 | AGRI_RAT |
| 15 | 37 | 74.0 | 53 | 1 | IOVO_FRACO |
| 16 | 36 | 72.0 | 351 | 1 | DPGN_DIPWA |
| 17 | 36 | 72.0 | 684 | 1 | RIAB_CVPPU |
| 18 | 36 | 72.0 | 6781 | 1 | RIAB_PEDV7 |
| 19 | 35 | 70.0 | 79 | 1 | IPK2_RAT |
| 20 | 35 | 70.0 | 93 | 1 | VNEP_PVSP |
| 21 | 35 | 70.0 | 140 | 1 | VNEP_LSV |
| 22 | 35 | 70.0 | 1154 | 1 | KDGD_MESAU |
| 23 | 33 | 66.0 | 54 | 1 | IOVO_GEOCA |
| 24 | 32 | 64.0 | 223 | 1 | KITH_UREFA |
| 25 | 32 | 64.0 | 806 | 1 | BIMA_EMENI |
| 26 | 32 | 64.0 | 1955 | 1 | AGRI_CHICK |
| 27 | 31.5 | 63.0 | 759 | 1 | PMT6_YEAST |
| 28 | 31 | 62.0 | 48 | 1 | IELA_ANESU |
| 29 | 31 | 62.0 | 53 | 1 | IOVO_ARBTO |
| 30 | 31 | 62.0 | 53 | 1 | IOVO_PRAAF |
| 31 | 31 | 62.0 | 56 | 1 | IOVO_PRAER |
| 32 | 31 | 62.0 | 81 | 1 | IAC_MACFA |
| 33 | 31 | 62.0 | 84 | 1 | IAC2_HUMAN |

ALIGNMENTS

RESULT 1

| ID | IPK1_HORSE | STANDARD; | PRT; | 56 AA. |
|----|---|-----------|------|--------|
| AC | P81634; | | | |
| DT | 15-JUL-1999 (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Pancreatic secretory trypsin inhibitor. | | | |
| GN | SPINK1 OR PSTI. | | | |
| OS | Equus caballus (Horse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Perissodactyla; Equidae; Equus. | | | |
| OX | NCBI_TaxID=9796; | | | |
| RN | [1] | | | |
| RP | SEQUENCE. | | | |
| RC | TISSUE=Pancreas; | | | |
| RA | Voit J.; | | | |
| RT | "Representation and characterization of pancreatic secretory | | | |
| RT | proteinase inhibitors from various animal species."; | | | |
| RL | Thesis (1993), Ludwig-Maximilians University / Munich, Germany. | | | |
| CC | -!- FUNCTION: This is a trypsin inhibitor, its physiological function | | | |
| CC | is to prevent the trypsin-catalyzed premature activation of | | | |
| CC | zymogens within the pancreas. | | | |
| CC | -!- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -!- SIMILARITY: Contains 1 Kazal-like domain. | | | |
| DR | HSP; P37109; IPCE. | | | |
| DR | InterPro; IPR002350; Kazal. | | | |
| DR | InterPro; IPR001239; Kazal_inhib. | | | |
| DR | Pfam; PF00050; Kazal; 1. | | | |
| DR | PRINTS; PR00290; KAZALINHTR. | | | |
| DR | SMART; SM00280; KAZAL; 1. | | | |
| DR | PROSITE; PS00282; KAZAL; 1. | | | |
| KW | Serine protease inhibitor. | | | |
| FT | DOMAIN 7 56 | | | |
| FT | DISULFID 9 38 | | | |
| FT | DISULFID 16 35 | | | |
| FT | DISULFID 24 56 | | | |
| FT | ACT SITE 18 19 | | | |
| SQ | SEQUENCE 56 AA; 6093 MW; D0DAAVE4FDB507E0 CRC64; | | | |

Query Match 88.0%; Score 44; DB 1; Length 56;

Best Local Similarity 70.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGXXIYXPCV 11

Db 15 GCTKIYNPVC 24

RESULT 2

| ID | IPK1_HUMAN | STANDARD; | PRT; | 79 AA. |
|----|---|-----------|------|--------|
| ID | IPK1_HUMAN | | | |
| AC | P00995; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 01-MAR-1989 (Rel. 10, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |

DE Pancreatic secretory trypsin inhibitor precursor (Tumor-associated
DE trypsin inhibitor) (TATI) (Serine protease inhibitor Kazal-type 1).
GN SPINK1 OR PSTI.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86106485; PubMed=3501289;
RA Horii A., Kobayashi T., Tomita N., Yamamoto T., Fukushima S.,
RA Murotsu T., Ogawa M., Mori T., Matsubara K.;
RT "Primary structure of human pancreatic secretory trypsin inhibitor
RT (PSTI) gene";
RL Biochem. Biophys. Res. Commun. 149:635-641(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86050645; PubMed=3877508;
RA Yamamoto T., Nakamura Y., Nishide T., Emi M., Ogawa M., Mori T.,
RA Matsubara K.;
RT "Molecular cloning and nucleotide sequence of human pancreatic
RT secretory trypsin inhibitor (PSTI) cDNA";
RL Biochem. Biophys. Res. Commun. 132:605-612(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88083571; PubMed=2961612;
RA Tomita N., Horii A., Yamamoto T., Ogawa M., Mori T., Matsubara K.;
RT "Expression of pancreatic secretory trypsin inhibitor gene in
RT neoplastic tissues";
RL FEBS Lett. 225:113-119(1987).
RN [4]
RP SEQUENCE FROM N.A., VARIANTS HPC PRO-14 AND SER-34, AND VARIANT
RP SER-55.
RX MEDLINE=20296628; PubMed=10835640;
RA Witt H., Luck W., Hennies H.C., Classen M., Kage A., Lass U.,
RA Landt O., Becker M.;
RT "Mutations in the gene encoding the serine protease inhibitor, Kazal
RT type 1 are associated with chronic pancreatitis";
RL Nat. Genet. 25:213-216(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 24-79.
RX MEDLINE=77131145; PubMed=843082;
RA Bartelt D.C., Shapanka R., Greene L.J.;
RT "The primary structure of the human pancreatic secretory trypsin
RT inhibitor. Amino acid sequence of the reduced S-aminoethylated
RT protein";
RL Arch. Biochem. Biophys. 179:189-199(1977).
RN [7]
RP SEQUENCE OF 24-46.

RX MEDLINE=83056875; PubMed=7142173;
RA Huhtala M.-L., Pesonen K., Kalkkinen N., Stenman U.-H.;
RT "Purification and characterization of a tumor-associated trypsin
RT inhibitor from the urine of a patient with ovarian cancer";
RL J. Biol. Chem. 257:13713-13716(1982).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92309406; PubMed=1613792;
RA Hecht H.-J., Szardenings M., Collins J., Schomburg D.;
RT "Three-dimensional structure of a recombinant variant of human
RT pancreatic secretory trypsin inhibitor (Kazal type)";
RL J. Mol. Biol. 225:1095-1103(1992).
RN [9]
RP STRUCTURE BY NMR OF MUTANT LEU-41/ARG-44.
RX MEDLINE=93164251; PubMed=8433367;
RA Klaus W., Schomburg D.;
RT "Solution structure of a variant of human pancreatic secretory
RT trypsin inhibitor determined by nuclear magnetic resonance
RT spectroscopy";
RL J. Mol. Biol. 229:695-706(1993).
RN [10]
RP VARIANT HPC SER-34, AND VARIANT SER-55.
RX MEDLINE=20144835; PubMed=10691414;
RA Chen J.-M., Mercier B., Audrezet M.-P., Ferec C.;
RT "Mutational analysis of the human pancreatic secretory trypsin
RT inhibitor (PSTI) gene in hereditary and sporadic chronic
RT pancreatitis";
RL J. Med. Genet. 37:67-69(2000).
CC -1- FUNCTION: This is a trypsin inhibitor, its physiological function
CC is to prevent the trypsin-catalyzed premature activation of
CC zymogens within the pancreas.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Defects in SPINK1 are a cause of hereditary pancreatitis,
CC (HPC); also known as chronic pancreatitis (CP). HPC is an
CC autosomal dominant disease characterized by the presence of
CC calculi in pancreatic ducts. It causes severe abdominal pain
CC attacks.
CC -1- SIMILARITY: Contains 1 Kazal-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20530; AAA36522.1; -;
DR EMBL; M22971; AAA36522.1; JOINED.
DR EMBL; M20528; AAA36522.1; JOINED.
DR EMBL; M20529; AAA36522.1; JOINED.
DR EMBL; Y00705; AAA68697.1; -;
DR EMBL; M1949; AAA36521.1; -;
DR EMBL; AF286028; AAG00531.1; -;
DR EMBL; BC025790; AAH25790.1; -;
DR PIR; A27484; TITHUA.
DR PDB; 1HPT; 31-OCT-93.
DR Genew; HGNC:11244; SPINK1.
DR MIM; 167790; -;
DR MIM; 167800; -;
DR GO; GO:0004966; F:Endopeptidase inhibitor activity; TAS.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00290; KAZALINHTR.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Serine protease inhibitor; Signal; Disease mutation; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 79 PANCREATIC SECRETORY TRYPsin INHIBITOR.
FT DOMAIN 30 79 KAZAL-LIKE.
FT DISULFID 32 61

Query Match 84.0%; Score 42; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.036; 3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPVC 11
DB 15 GCPRIYNPVC 24

RESULT 4
ID IPK1 PIG STANDARD; PRT; 56 AA.
AC P00998;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor.
GN SPINK1 OR PSTI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70283430; PubMed=5466061;
TS Tschesche H., Wachter E.;
RT "The structure of the porcine pancreatic secretory trypsin inhibitor.
RT I. A sequence determination by Edman degradation and mass spectral
RT identification of the p-bromophenyl-thiohydantoins.";
RL Eur. J. Biochem. 16:187-198(1970).
RN [2]
RP SEQUENCE.
RX MEDLINE=71178430; PubMed=5103069;
RA Bartelt D.C., Greene L.J.;
RT "The primary structure of the porcine pancreatic secretory trypsin
RT inhibitor. I. Amino acid sequence of the reduced S-aminoethylated
RT protein.";
RL J. Biol. Chem. 246:2218-2229(1971).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=73001409; PubMed=4672150;
RA Tschesche H., Schneider M., Reidel G., Klein H.;
RT "Disulfide bridges of the secretory trypsin inhibitor from porcine
RT pancreas and the degradation of covalent structure during the
RT temporary inhibition.";
RL Hoppe-Seyler's Z. Physiol.-Chem. 353:763-764(1972).
RN [4]
RP SEQUENCE OF A SECOND INHIBITOR.
RX MEDLINE=71092915; PubMed=5531651;
RA Tschesche H., Wachter E.;
RT "Trypsin inhibitors. VII. Primary structure of the specific trypsin
RT inhibitor II (Kazal-type) from porcine pancreas. Sequence analysis
RT with mass spectrometry identification of the Edman degradation.";
RL p-bromophenylthio-hydantoins from the Edman degradation.";
RN Hoppe-Seyler's Z. Physiol. Chem. 351:1449-1459(1970).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=83189075; PubMed=7169635;
RA Bolognesi M., Gatti G., Menegatti E., Guarneri M., Marquart M.,
RA Papamokos E., Huber R.;
RT "Three-dimensional structure of the complex between pancreatic
RT secretory trypsin inhibitor (Kazal type) and trypsinogen at 1.8-A
RT resolution. Structure solution, crystallographic refinement and
RT preliminary structural interpretation.";
RL J. Mol. Biol. 182:839-868(1982).
CC -1- FUNCTION: This is a trypsin inhibitor, its physiological function
CC is to prevent the trypsin-catalyzed premature activation of
CC zymogens within the pancreas.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 Kazal-like domain.
DR PIR; A91174; TIFG.
DR PDB; 1TGS; 14-MAR-85.
DR InterPro; IPR002350; kazal.

Query Match 88.0%; Score 44; DB 1; Length 79;
Best Local Similarity 70.0%; Pred. No. 0.02; 3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPVC 11
DB 38 GCTKIYDVC 47

ULT 3
1-BOVIN
ID IPK1 BOVIN STANDARD; PRT; 56 AA.
AC P00996;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor.
GN SPINK1 OR PSTI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=69187206; PubMed=5769997;
TS Greene L.J., Bartelt D.C.;
RT "The structure of the bovine pancreatic secretory trypsin inhibitor --
RT Kazal's inhibitor. II. The order of the tryptic peptides.";
RL J. Biol. Chem. 244:2646-2657(1969).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=72086018; PubMed=5135319;
Guy O., Shapanka R., Greene L.J.;
RT "The structure of the bovine pancreatic secretory trypsin inhibitor --
RT Kazal's inhibitor. 3. Determination of the disulfide bonds and
RT proteolysis by thermolysin.";
RL J. Biol. Chem. 246:7740-7747(1971).
CC -1- FUNCTION: This is a trypsin inhibitor, its physiological function
CC is to prevent the trypsin-catalyzed premature activation of
CC zymogens within the pancreas.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 Kazal-like domain.
DR PIR; A01230; TIBOA.
DR HSSP; P37109; 1PCE.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00280; KAZALINHTR.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
DR Serine protease inhibitor.
DR DOMAIN 7 56 KAZAL-LIKE.
DR DISULFID 9 38
DR DISULFID 16 35
DR DISULFID 24 56
DR ACT SITE 18 19
DR REACTIVE BOND.
DR AB64A512AC851B26 CRC64;
SEQUENCE 56 AA; 6161 MW; AB64A512AC851B26 CRC64;

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DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00290; KAZALINHBTR.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Serine protease inhibitor; 3D-structure.
FT DOMAIN 7 56
FT DISULFID 9 38
FT DISULFID 16 35
FT DISULFID 24 56
FT ACT_SITE 18 19
FT VARIANT 1 4
FT STRAND 16 17
FT STRAND 23 25
FT TURN 26 27
FT STRAND 30 31
FT HELIX 34 42
FT TURN 43 43
FT STRAND 50 53
SQ SEQUENCE 56 AA; 6023 MW; 39A3649DADF16D25 CRC64;

Query Match 84.0%; Score 42; DB 1; Length 56;
Best Local Similarity 70.0%; Pred. No. 0.036;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPC 11
DB 15 GCPRIYNPVC 24

RESULT 5
IPK1 SHEEP STANDARD; PRT; 56 AA.
AC P00977;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor.
GN SPINK1 OR PSTI.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP PARTIAL SEQUENCE.
RA Tschesche H., Obermeier R., Hochstrasser K.;
RL Unpublished results, cited by;
RL Tschesche H., Wachter E., Kupfer S., Obermeier R., Reidel G.,
RL Haenisch G., Schneider M.;
RL (In) Fritz H., Tschesche H. (eds.);
RL Proceedings of the international research conference on proteinase
RL inhibitors, pp.207-222, Walter de Gruyter, New York (1971).
CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function
CC is to prevent the trypsin-catalyzed premature activation of
CC zymogens within the pancreas.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This protein is unusual, with respect to the other
CC mammalian PSTI proteins, in having an extra N-terminal residue.
CC -!- SIMILARITY: Contains 1 Kazal-like domain.
DR PIR; A01232; TIDGA.
DR HSSP; P37109; 1PCE.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00290; KAZALINHBTR.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Serine protease inhibitor.
FT DOMAIN 8 57
FT DISULFID 10 39
FT DISULFID 17 36
FT DISULFID 25 57
FT ACT_SITE 19 20
SQ SEQUENCE 57 AA; 6319 MW; 2DB674A2FD98CD43 CRC64;

Query Match 84.0%; Score 42; DB 1; Length 57;
Best Local Similarity 60.0%; Pred. No. 0.037;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPC 11
DB 16 GCKIYNPIC 25

RESULT 6
IPK1 CANPA STANDARD; PRT; 57 AA.
AC P04542;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor.
GN SPINK1 OR PSTI.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=86030679; PubMed=4054311;
RA Kikuchi N., Nagata K., Yoshida N., Tanaka T., Yamamoto M., Saitoh Y.;
RT "Purification and complete amino acid sequence of canine pancreatic
RT secretory trypsin inhibitor.";
RL FEBS Lett. 191:269-272(1985).
CC -!- FUNCTION: This is a trypsin inhibitor, its physiological function
CC is to prevent the trypsin-catalyzed premature activation of
CC zymogens within the pancreas.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This protein is unusual, with respect to the other
CC mammalian PSTI proteins, in having an extra N-terminal residue.
CC -!- SIMILARITY: Contains 1 Kazal-like domain.
DR PIR; A01232; TIDGA.
DR HSSP; P37109; 1PCE.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00290; KAZALINHBTR.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Serine protease inhibitor.
FT DOMAIN 8 57
FT DISULFID 10 39
FT DISULFID 17 36
FT DISULFID 25 57
FT ACT_SITE 19 20
SQ SEQUENCE 57 AA; 6319 MW; 2DB674A2FD98CD43 CRC64;

Query Match 84.0%; Score 42; DB 1; Length 57;
Best Local Similarity 60.0%; Pred. No. 0.037;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIYXPC 11
DB 16 GCKIYNPIC 25

RESULT 7
IPK1 RAT STANDARD; PRT; 79 AA.
AC P09655; P13072;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pancreatic secretory trypsin inhibitor I precursor (PSTI-I)
DE (cholecystokinin-releasing peptide) (Monitor peptide).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

```

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Pancreas;
 MEDLINE=90098786; PubMed=2602119;
 Fukuda S.-I., Scheele G.A.;
 "Complementary nucleotide sequence for monitor peptide, a novel
 cholecystokinin-releasing peptide in the rat.";
 Nucleic Acids Res. 17:10111-10111(1989).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=Wistar; TISSUE=Pancreas;
 MEDLINE=90083122; PubMed=2293709;
 Fukuda S.-I., Scheele G.A.;
 "Rapid and selective cloning of monitor peptide, a novel
 cholecystokinin-releasing peptide, using minimal amino acid sequence
 and the polymerase chain reaction.";
 Pancreas 5:1-7(1990).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Pancreas;
 MEDLINE=8932236; PubMed=2751646;
 Horii A., Tomita N., Yokouchi H., Doi S., Uda K., Ogawa M., Mori T.,
 Matsubara K.;
 "On the cDNA's for two types of rat pancreatic secretory trypsin
 inhibitor.";
 Biochem. Biophys. Res. Commun. 162:151-159(1989).
 [4]
 SEQUENCE FROM N.A.
 MEDLINE=91293130; PubMed=2065678;
 Tezuka S., Fushiki T., Kondo A., Murayama H., Sugimoto E.;
 "Effect of a high-protein diet on the gene expression of a trypsin-
 sensitive, cholecystokinin-releasing peptide (monitor peptide) in the
 pancreas.";
 Eur. J. Biochem. 199:245-252(1991).
 [5]
 SEQUENCE FROM N.A.
 MEDLINE=93003324; PubMed=1390891;
 Tezuka S., Miura Y., Fushiki T., Oomori T., Satoh T., Natori Y.,
 Sugimoto E.;
 "Molecular cloning and characterization of genes encoding rat
 pancreatic cholecystokinin (CCK)-releasing peptide (monitor peptide)
 and pancreatic secretory trypsin inhibitor (PSTI).";
 Biochim. Biophys. Acta 1132:199-202(1992).
 [6]
 SEQUENCE OF 19-79.
 STRAIN=Wistar; TISSUE=Pancreas;
 MEDLINE=89076534; PubMed=3202973;
 Uda K., Ogawa M., Shibata T., Murata A., Mori T., Kikuchi N.,
 Yoshida N., Tsunawasa S., Sakiyama F.;
 "Purification, characterization and amino-acid sequencing of two
 pancreatic secretory trypsin inhibitors in rat pancreatic juice.";
 Biol. Chem. Hoppe-Seyler 369:55-61(1988).
 [7]
 SEQUENCE OF 19-79.
 TISSUE=Pancreas;
 MEDLINE=87250528; PubMed=3597401;
 Iwai K., Fukuda S.-I., Fushiki T., Tsujikawa M., Hirose M.,
 Tsunawasa S., Sakiyama F.;
 "Purification and sequencing of a trypsin-sensitive cholecystokinin-
 releasing peptide from rat pancreatic juice. Its homology with
 pancreatic secretory trypsin inhibitor.";
 J. Biol. Chem. 262:8956-8959(1987).
 -!- FUNCTION: This is a trypsin inhibitor, its physiological function
 is to prevent the trypsin-catalyzed premature activation of
 zymogens within the pancreas.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- SIMILARITY: Contains 1 Kazal-like domain.

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 or send an email to license@isb-sib.ch).

 CC EMBL; X59696; CAA42217.1; -;
 CC EMBL; M22162; AAA41629.1; -;
 CC EMBL; M35299; AAA47479.1; -;
 CC EMBL; M35300; AAA41977.1; -;
 CC EMBL; M27882; AAA41975.1; -;
 CC EMBL; D11321; BAA01944.1; -;
 CC PIR; S09602; TIRTL.
 CC HSSP; P37109; IPCE.
 CC InterPro; IPR002350; Kazal.
 CC InterPro; IPR001239; Kazal_inhib.
 CC Pfam; PF00050; Kazal; 1.
 CC PRINTS; PR00290; KAZALINHTR.
 CC SMART; SM00280; KAZAL; 1.
 CC PROSITE; PS00282; KAZAL; 1.
 CC Serine protease inhibitor; Signal.
 CC SIGNAL 1 18 PANCREATIC SECRETORY TRYPSIN INHIBITOR I.
 CC CHAIN 19 79 KAZAL-LIKE.
 CC DOMAIN 30 79 BY SIMILARITY.
 CC DISULFID 32 61 BY SIMILARITY.
 CC DISULFID 39 58 BY SIMILARITY.
 CC DISULFID 47 79 REACTIVE BOND.
 CC ACT_SITE 41 42 T -> G (IN REF. 7).
 CC CONFLICT 78 78
 CC SEQUENCE 79 AA; 8528 MW; 5816D55DF7B57874 CRC64;
 SQ
 Query Match 84.0%; Score 42; DB 1; Length 79;
 Best Local Similarity 70.0%; Pred. No. 0.05;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GCXXIXXPVC 11
 Db 38 GCPRIYDVC 47

 RESULT 8
 ISK3 MOUSE
 ID -ISK3_MOUSE STANDARD; PRT; 80 AA.
 AC P09036;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine protease inhibitor Kazal-type 3 precursor (Prostatic secretory
 DE glycoprotein) (P12).
 DE GN SPINK3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=88111560; PubMed=3428272;
 RA Mills J.S., Needham M., Parker M.G.;
 RT "A secretory protease inhibitor requires androgens for its expression
 RT in male sex accessory tissues but is expressed constitutively in
 RT pancreas.";
 RL EMBO J. 6:3711-3717(1987).
 CC -!- FUNCTION: SERINE PROTEASE INHIBITOR WHICH EXHIBITS ANTI-TRYPSIN
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: By androgens.
 CC -!- SIMILARITY: Contains 1 Kazal-like domain.

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JUL 11
1 PIG
5 CSLIYAPVC 13

1 SK4 PIG STANDARD; PRT; 86 AA.
P37109;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine protease inhibitor Kazal-type 4 precursor (Peptide PEC-60).
SPINK4.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
MEDLINE=93015834; PubMed=1400298;
Metsis M., Cintra A., Solfrini V., Ernfors P., Bortolotti F.,
Morrauttti D.G., Ostenson C.-G., Efendic S., Agerberth B., Mutt V.,
Persson H., Fuxe K.;
"Molecular cloning of PEC-60 and expression of its mRNA and peptide
in the gastrointestinal tract and immune system.";
J. Biol. Chem. 267:19829-19832(1992).
[2]
SEQUENCE OF 27-86.
TISSUE=Intestine;
MEDLINE=90046843; PubMed=2573065;
Agerberth B., Soederling-Barros J., Joernvall H., Chen Z.,
Ostenson C.G., Efendic S., Mutt V.;
"Isolation and characterization of a 60-residue intestinal peptide
structurally related to the pancreatic secretory type of trypsin
inhibitor: influence on insulin secretion.";
Proc. Natl. Acad. Sci. U.S.A. 86:8590-8594(1989).
[3]
STRUCTURE BY NMR.
MEDLINE=94254085; PubMed=8196042;
Ljepinch E., Berndt K.D., Sillard R., Mutt V., Otting G.;
"Solution structure and dynamics of PEC-60, a protein of the Kazal
type inhibitor family, determined by nuclear magnetic resonance
spectroscopy.";
J. Mol. Biol. 239:137-153(1994).
-1- FUNCTION: Inhibits the glucose-induced insulin secretion from
perfused pancreas; also plays a role in the immune system. Does
not inhibit trypsin.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: SYNTHESIZED IN DUODENAL GOBLET CELLS AND
IN MONOCYTES IN BONE MARROW AND BLOOD.
-1- SIMILARITY: Contains 1 Kazal-like domain.

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or send an email to license@ebi.ac.uk).

EMBL; S46866; AAB23691.2; -;
EMBL; X67109; CAA47482.1; -;
PIR; A44041; A34427.
PIR; LPCE; 30-APR-94.
PDB; 1PCE; 30-APR-94.
InterPro; IPR002350; kazal.
InterPro; IPR001239; Kazal_inhib.
Pfam; PF00050; kazal; 1.
PRINTS; PR00280; KAZALINHTR.
SMART; SMO0280; KAZAL; 1.
PROSITE; PS00282; KAZAL; 1.
3D-structure; Signal.
SIGNAL 1 26
CHAIN 27 86 SERINE PROTEASE INHIBITOR KAZAL-TYPE 4.

FT DOMAIN 35 86
FT DISULFID 37 68
FT DISULFID 46 65
FT DISULFID 54 86
FT ACT_SITE 48 49
FT TURN 29 30
FT STRAND 33 33
FT TURN 41 42
FT TURN 47 48
FT STRAND 53 55
FT TURN 56 57
FT STRAND 60 61
FT HELIX 64 74
FT TURN 75 75
FT STRAND 80 83
SQ SEQUENCE 86 AA; 9635 MW; 5D513142CF3A4B4D CRC64;
Query Match 76.0%; Score 38; DB 1; Length 86;
Best Local Similarity 66.7%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CXXIYXPVC 11
Db 46 CSRIYDFVC 54

RESULT 12

ESM1 DROME STANDARD; PRT; 156 AA.
ID ESM1 DROME STANDARD; PRT; 156 AA.
AC 037176;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Enhancer of split M1 protein precursor (E(sp1)m1).
GN M1 OR CG8342.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=99173785; PubMed=10072784;
RA Wurmbach E., Wech I., Preiss A.;
"The enhancer of split complex of Drosophila melanogaster harbors
three classes of Notch responsive genes.";
Mech. Dev. 80:171-180(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari P., Bhatnagar S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE TIME WHEN SEPARATION OF
 CC NEURAL AND EPIDERMAL PRECURSORS CELLS OCCURS. ACCUMULATES
 CC TRANSIENTLY AT THE FUSION SITES OF ANTERIOR AND POSTERIOR MIDGUT
 CC AND VERY SPECIFICALLY TO HIGH LEVELS IN THE PROVENTRICULUS OF THE
 CC EMERYO.
 CC -!- SIMILARITY: Contains 1 kazal-like domain.
 CC -----
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 CC -----
 CC EMBL; AJ010167; CAB39163.1; -;
 DR EMBL; AE003754; AAF56548.1; -;
 DR Flybase; FBgn0002578; ml.
 DR InterPro; IPR002350; kazal.
 DR Pfam; PF00050; kazal; 1.
 DR SMART; SM00280; KAZAL; 2.
 DR PROSITE; PS00282; KAZAL; FALSE NEG.
 KW Serine protease inhibitor; Differentiation; Neurogenesis; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 156 ENHANCER OF SPLIT M1 PROTEIN.
 FT DOMAIN 29 75 KAZAL-LIKE.
 FT SEQUENCE 156 AA; 17339 MW; 5C29P73AE89F6949 CRC64;
 Query Match 76.0%; Score 39; DB 1; Length 156;
 Best Local Similarity 66.7%; Pred. No. 0.64;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 CXXYXPVC 11
 Db 106 CSMIYQVPC 114
 ID -IOV7 CHICK STANDARD; PRT; 472 AA.
 AC P10184;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ovoidinhibitor precursor.
 GN OIK.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-472.
 RX MEDLINE=87194792; PubMed=3571241;
 RA Scott M.J., Huckaby C.S., Kato I., Kohr W.J., Laskowski M. Jr.,
 RA Tsai M.-J., O'Malley B.W.;

RT "Ovoidinhibitor introns specify functional domains as in the related
 RT and linked ovomucoid gene.";
 RL J. Biol. Chem. 262:5839-5907(1987).
 CC -!- FUNCTION: SEEMS TO HAVE AT LEAST FIVE ACTIVE INHIBITORY DOMAINS;
 CC TWO FOR TRYPSIN, TWO FOR CHYMOTRYPSIN AND ONE FOR ELASTASE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EGG WHITE AND PLASMA.
 CC -!- SIMILARITY: Contains 7 kazal-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M16141; AAA48994.1; -;
 DR EMBL; M15962; AAA48994.1; JOINED.
 DR EMBL; M16127; AAA48994.1; JOINED.
 DR EMBL; M16128; AAA48994.1; JOINED.
 DR EMBL; M16123; AAA48994.1; JOINED.
 DR EMBL; M16130; AAA48994.1; JOINED.
 DR EMBL; M16131; AAA48994.1; JOINED.
 DR EMBL; M16132; AAA48994.1; JOINED.
 DR EMBL; M16133; AAA48994.1; JOINED.
 DR EMBL; M16134; AAA48994.1; JOINED.
 DR EMBL; M16135; AAA48994.1; JOINED.
 DR EMBL; M16136; AAA48994.1; JOINED.
 DR EMBL; M16137; AAA48994.1; JOINED.
 DR EMBL; M16138; AAA48994.1; JOINED.
 DR EMBL; M16139; AAA48994.1; JOINED.
 DR EMBL; M16140; AAA48994.1; JOINED.
 DR PIR; A26730; A26730.
 DR HSSP; P05586; ZOVO.
 DR InterPro; IPR002350; kazal.
 DR Pfam; PF00050; kazal; 7.
 DR PRINTS; PR00290; KAZALINHBTR.
 DR SMART; SM00280; KAZAL; 7.
 DR PROSITE; PS00282; KAZAL; 7.
 KW Serine protease inhibitor; Repeat; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 472 OVOIDINHIBITOR.
 FT DOMAIN 26 91 KAZAL-LIKE 1.
 FT DOMAIN 92 156 KAZAL-LIKE 2.
 FT DOMAIN 157 222 KAZAL-LIKE 3.
 FT DOMAIN 223 287 KAZAL-LIKE 4.
 FT DOMAIN 288 353 KAZAL-LIKE 5.
 FT DOMAIN 354 419 KAZAL-LIKE 6.
 FT DOMAIN 412 472 KAZAL-LIKE 7.
 FT ACT_SITE 47 48 REACTIVE BOND 1 (POSSIBLY TRYPSIN).
 FT ACT_SITE 112 113 REACTIVE BOND 2 (POSSIBLY TRYPSIN).
 FT ACT_SITE 178 179 REACTIVE BOND 3 (POSSIBLY TRYPSIN).
 FT ACT_SITE 244 245 REACTIVE BOND 4 (POSSIBLY TRYPSIN).
 FT ACT_SITE 309 310 REACTIVE BOND 5 (POSSIBLY CHYMOTRYPSIN).
 FT ACT_SITE 375 376 REACTIVE BOND 6 (POSSIBLY CHYMOTRYPSIN
 AND ELASTASE).
 FT ACT_SITE 434 435 REACTIVE BOND 7 (POSSIBLY CHYMOTRYPSIN
 AND ELASTASE).
 FT DISULFID 28 67
 FT DISULFID 45 64
 FT DISULFID 53 85
 FT DISULFID 94 132
 FT DISULFID 110 129
 FT DISULFID 118 150
 FT DISULFID 159 198
 FT DISULFID 176 195
 FT DISULFID 184 216
 FT DISULFID 225 264
 FT DISULFID 242 261
 FT DISULFID 250 282
 FT DISULFID 291 329

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DISULFID 307 326
DISULFID 315 347
DISULFID 356 395
DISULFID 373 392
DISULFID 381 413
DISULFID 422 454
DISULFID 432 451
DISULFID 440 472
CONFLICT 333 333
SEQUENCE 472 AA; 51919 MW; A30211B297B800E5 CRC64;
MISSING (IN REF. 1; AA SEQUENCE).
very Match 76.0%; Score 38; DB 1; Length 472;
st Local Similarity 66.7%; Pred. No. 1.9;
atches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPCV 11
373 CTWYDPCV 381

ILT 14
: RAT
: AGRI RAT STANDARD; PRT; 1959 AA.
P25304; Q63034;
01-MAY-1992 (Rel. 22, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agrin precursor.
AGRN.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
TISSUE=Embryonic spinal cord;
MEDLINE=91222570; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
"Structure and chromosomal localization of the mammalian agrin gene.";
J. Neurosci. 12:3535-3544(1992).
-i- FUNCTION: Component of the basal lamina that causes the
aggregation of acetylcholine receptors and acetylcholine-esterase
on the surface of muscle fibers of the neuromuscular junction.
-i- SUBUNIT: Binds to laminin.
-i- SUBCELLULAR LOCATION: Synaptic basal lamina at the neuromuscular
junction.
-i- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist. Isoforms differ in
their acetylcholine receptor clustering activity;
Name=1;
IsoId=P25304-1; Sequence=Displayed;
Name=2;
IsoId=P25304-2; Sequence=VSP_001365;
Name=3;
IsoId=P25304-3; Sequence=VSP_001366;
Name=4;
IsoId=P25304-4; Sequence=VSP_001367;
Name=5;
IsoId=P25304-5; Sequence=VSP_001368;
-i- TISSUE SPECIFICITY: Embryonic nervous system and muscle.
-i- DEVELOPMENTAL STAGE: More abundant early in development.
-i- PTM: Contains heparan sulfate chains as well as N-linked and O-
linked oligosaccharides (By similarity).
-i- SIMILARITY: Contains 9 Kazal-like domains.
-i- SIMILARITY: Contains 2 laminin EGF-like domains.
-i- SIMILARITY: Contains 4 EGF-like domains.

CC -1- SIMILARITY: Contains 1 SEA domain.
CC -1- SIMILARITY: Contains 3 laminin G-like domains.
CC -1- CAUTION: It is uncertain whether Met-1, Met-18 or Met-24 is the
CC initiator.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M64780; AAA40703.1;
CC EMBL; M64780; AAA40702.1; ALT_INIT.
CC EMBL; S44194; AAB23326.1;
CC PIR; JH0399; AGRT.
CC HSP; P00740; LEDM.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR003645; FOLN.
CC InterPro; IPR002350; kazal.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR000082; SEA_domain.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00050; kazal; 9.
CC Pfam; PF00053; laminin_EGF; 2.
CC Pfam; PF00054; laminin_G; 3.
CC Pfam; PF01390; SEA; 1.
CC PRINTS; PR00011; EGF/LAMININ.
CC SMART; SM00180; EGF_Lam; 2.
CC SMART; SM00274; FOLN; 8.
CC SMART; SM00280; KAZAL; 9.
CC SMART; SM00282; LamG; 3.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS00022; EGF_1; 6.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50026; EGF_3; 4.
CC PROSITE; PS50025; LAM G DOMAIN; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
CC PROSITE; PS50024; SEA; 1.
KW Glycoprotein; EGF-like domain; Repeat; Alternative splicing; Signal;
KW Laminin EGF-like domain; Proteoglycan; Heparan sulfate.
FT SIGNAL 1 29
FT CHAIN 30 1959
FT DOMAIN 65 137 KAZAL-LIKE 1.
FT DOMAIN 141 212 KAZAL-LIKE 2.
FT DOMAIN 213 284 KAZAL-LIKE 3.
FT DOMAIN 287 356 KAZAL-LIKE 4.
FT DOMAIN 361 429 KAZAL-LIKE 5.
FT DOMAIN 430 494 KAZAL-LIKE 6.
FT DOMAIN 495 559 KAZAL-LIKE 7.
FT DOMAIN 563 645 KAZAL-LIKE 8.
FT DOMAIN 688 741 LAMININ_EGF-LIKE 1.
FT DOMAIN 742 786 LAMININ_EGF-LIKE 2.
FT DOMAIN 794 864 KAZAL-LIKE 9.
FT DOMAIN 1023 1145 SEA.
FT DOMAIN 1220 1258 EGF-LIKE 1.
FT DOMAIN 1263 1439 LAMININ_G-LIKE 1.
FT DOMAIN 1440 1477 EGF-LIKE 2.
FT DOMAIN 1479 1516 EGF-LIKE 3.
FT DOMAIN 1526 1708 LAMININ_G-LIKE 2.
FT DOMAIN 1709 1748 EGF-LIKE 4.
FT DOMAIN 1784 1956 LAMININ_G-LIKE 3.
FT DOMAIN 869 992 SER/THR-RICH.
FT DOMAIN 1147 1215 SER/THR-RICH.
FT DISULFID 97 116
FT DISULFID 105 137
FT DISULFID 171 191
FT DISULFID 180 212
FT DISULFID 244 263
FT DISULFID 252 284

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FT DISULFID 316 335 POTENTIAL.
FT DISULFID 324 356 POTENTIAL.
FT DISULFID 389 408 POTENTIAL.
FT DISULFID 397 429 POTENTIAL.
FT DISULFID 454 473 POTENTIAL.
FT DISULFID 462 494 POTENTIAL.
FT DISULFID 518 538 POTENTIAL.
FT DISULFID 527 559 POTENTIAL.
FT DISULFID 604 624 POTENTIAL.
FT DISULFID 613 645 POTENTIAL.
FT DISULFID 688 700 BY SIMILARITY.
FT DISULFID 690 707 BY SIMILARITY.
FT DISULFID 709 718 BY SIMILARITY.
FT DISULFID 721 739 BY SIMILARITY.
FT DISULFID 742 754 BY SIMILARITY.
FT DISULFID 744 761 BY SIMILARITY.
FT DISULFID 763 772 BY SIMILARITY.
FT DISULFID 775 786 BY SIMILARITY.
FT DISULFID 823 843 POTENTIAL.
FT DISULFID 832 864 POTENTIAL.
FT DISULFID 1224 1235 BY SIMILARITY.
FT DISULFID 1229 1246 BY SIMILARITY.
FT DISULFID 1248 1257 BY SIMILARITY.
FT DISULFID 1444 1455 POTENTIAL.
FT DISULFID 1449 1465 POTENTIAL.
FT DISULFID 1467 1476 POTENTIAL.
FT DISULFID 1483 1494 BY SIMILARITY.
FT DISULFID 1506 1515 BY SIMILARITY.
FT DISULFID 1713 1727 BY SIMILARITY.
FT DISULFID 1721 1736 BY SIMILARITY.
FT DISULFID 1738 1747 BY SIMILARITY.
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1144 1152 Missing (in isoform 2).
FT VARSPLIC 1780 1798 Missing (in isoform 3).
FT VARSPLIC 1788 1798 Missing (in isoform 4).
FT VARSPLIC 1780 1787 Missing (in isoform 5).
FT VARIANT 314 314 V -> VTCD (IN A VARIANT).
SQ SEQUENCE 1959 AA; 208645 MW; 7FEFDFDAFF89CC31 CRC64;

Query Match 76.0%; Score 38; DB 1; Length 1959;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXIIYXPVC 11
Db 389 CSGIYDPVC 397

RESULT 15
IOVO_FRACO STANDARD; PRT; 53 AA.
AC P05595;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ovomuroid (Fragment).
OS Francolinus coqui (Coqui francolin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Francolinus.
OX NCBI_TaxID=9021;
RN [1]
RP SEQUENCE.
RX MEDLINE=87157615; PubMed=3828298;
RA Laskowski M. Jr., Kato I., Ardelt W., Cook J., Denton A., Emple M.W.,

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RA Kohr W.J., Park S.J., Parks K., Schatzley B.L., Schoenberger O.L.,
RA Tashiro M., Vichot G., Whitley H.E., Wiczorek A., Wiczorek M.;
RT "Ovomucoid third domains from 100 avian species: isolation,
RT sequences, and hypervariability of enzyme-inhibitor contact
RT residues.";
RL Biochemistry 26:202-221(1987).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: AVIAN OVOMUCOID CONSIST OF THREE HOMOLOGOUS, TANDEM KAZAL
CC -1- FAMILY INHIBITORY DOMAINS.
CC -1- SIMILARITY: Contains 3 Kazal-like domains.
DR PIR; G31438; G31438.
DR HSSP; P05586; 4OVC.
DR InterPro; IPR002350; kazal.
DR InterPro; IPR001239; Kazal_inhib.
DR Pfam; PF00050; kazal; 1.
DR PRINTS; PR00290; KAZALINHBT.
DR SMART; SM00280; KAZAL; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Serine protease inhibitor; Glycoprotein; Repeat; Egg white.
FT NON_TER 1 1
FT DOMAIN 3 53 KAZAL-LIKE 3.
FT ACT_SITE 15 16 REACTIVE BOND 3.
FT DISULFID 5 35
FT DISULFID 13 32
FT DISULFID 21 53
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .).
FT NON_TER 53 53
SQ SEQUENCE 53 AA; 5739 MW; SEC6BEC58EDE7846 CRC64;

Query Match 74.0%; Score 37; DB 1; Length 53;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCXXIYXPVC 11
Db 12 GCTMEYRPVC 21

Search completed: August 11, 2004, 13:08:06
Job time : 8.38095 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: August 11, 2004, 13:04:18 ; Search time 35.0952 Seconds
(without alignments)
98,894 Million cell updates/sec

le: US-10-661-207-2
fect score: 50
ence: 1 XGCXIXXPVC 11

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues
al number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0
imum DB seq length: 200000000
:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- ibase :
- 1: sp_archea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| lt | o. | score | % Match | Query Length | DB Length | ID | Description |
|----|----|-------|------------|-----------------|--------------|--------------------|-------------|
| 1 | 43 | 86.0 | 155 | 5 | Q8T926 | Q8T926 tetrahymena | |
| 2 | 38 | 76.0 | 730 | 5 | Q9VNL6 | Q9VNL6 drosophila | |
| 3 | 37 | 74.0 | 56 | 6 | Q29185 | Q29185 sus scrofa | |
| 4 | 37 | 74.0 | 2026 | 4 | O00468 | O00468 homo sapien | |
| 5 | 36 | 72.0 | 94 | 5 | Q9VHK7 | Q9VHK7 drosophila | |
| 6 | 36 | 72.0 | 145 | 5 | Q9VES7 | Q9VES7 drosophila | |
| 7 | 36 | 72.0 | 1699 | 5 | O02037 | O02037 bdelloura c | |
| 8 | 35 | 70.0 | 140 | 12 | O36986 | O36986 lily sympto | |
| 9 | 35 | 70.0 | 140 | 12 | Q83090 | Q83090 lily sympto | |
| 10 | 35 | 70.0 | 222 | 5 | O95P16 | O95P16 triatoma in | |
| 11 | 35 | 70.0 | 385 | 4 | Q92659 | Q92659 homo sapien | |
| 12 | 35 | 70.0 | 406 | 16 | Q8F8E2 | Q8F8E2 leptospira | |
| 13 | 35 | 70.0 | 724 | 10 | Q9LXK8 | Q9LXK8 arabidopsis | |
| 14 | 34 | 68.0 | 82 | 12 | O91GK0 | O91GK0 epiphyas po | |
| 15 | 34 | 68.0 | 82 | 12 | Q7TLU0 | Q7TLU0 choristoneu | |
| 16 | 34 | 68.0 | 93 | 12 | O73509 | O73509 potato viru | |

| | | | | | | |
|----|----|------|------|----|--------|--------------------|
| 17 | 34 | 68.0 | 93 | 12 | O73529 | O73529 potato viru |
| 18 | 34 | 68.0 | 93 | 12 | O73531 | O73531 potato viru |
| 19 | 34 | 68.0 | 93 | 12 | O73512 | O73512 potato viru |
| 20 | 34 | 68.0 | 93 | 12 | O73508 | O73508 potato viru |
| 21 | 34 | 68.0 | 93 | 12 | O93139 | O93139 potato viru |
| 22 | 34 | 68.0 | 93 | 12 | O73514 | O73514 potato viru |
| 23 | 34 | 68.0 | 93 | 12 | O73527 | O73527 potato viru |
| 24 | 34 | 68.0 | 94 | 12 | O41486 | O41486 potato viru |
| 25 | 34 | 68.0 | 94 | 12 | O41484 | O41484 potato viru |
| 26 | 34 | 68.0 | 94 | 12 | O73525 | O73525 potato viru |
| 27 | 34 | 68.0 | 94 | 12 | O86541 | O86541 potato viru |
| 28 | 34 | 68.0 | 237 | 5 | Q25196 | Q25196 hydra atten |
| 29 | 34 | 68.0 | 321 | 10 | O84JM1 | O84JM1 arabidopsis |
| 30 | 34 | 68.0 | 335 | 10 | O9C559 | O9C559 arabidopsis |
| 31 | 34 | 68.0 | 341 | 5 | Q24329 | Q24329 drosophila |
| 32 | 34 | 68.0 | 341 | 5 | Q9VU62 | Q9VU62 drosophila |
| 33 | 34 | 68.0 | 366 | 5 | Q8SZW6 | Q8SZW6 drosophila |
| 34 | 34 | 68.0 | 405 | 11 | Q8C811 | Q8C811 mus musculu |
| 35 | 34 | 68.0 | 746 | 10 | O9SJ15 | O9SJ15 arabidopsis |
| 36 | 34 | 68.0 | 1120 | 4 | O9BX34 | O9BX34 homo sapien |
| 37 | 34 | 68.0 | 1164 | 4 | Q86XP2 | Q86XP2 homo sapien |
| 38 | 34 | 68.0 | 1220 | 4 | Q86XP1 | Q86XP1 homo sapien |
| 39 | 33 | 66.0 | 169 | 5 | O9U5B4 | O9U5B4 caenorhabdi |
| 40 | 33 | 66.0 | 274 | 16 | Q7UI56 | Q7UI56 rhodopirell |
| 41 | 33 | 66.0 | 279 | 5 | Q8T600 | Q8T600 plasmodium |
| 42 | 33 | 66.0 | 370 | 16 | O8A715 | O8A715 bacteroides |
| 43 | 33 | 66.0 | 757 | 10 | Q9SPJ0 | Q9SPJ0 oryza sativ |
| 44 | 33 | 66.0 | 759 | 10 | Q94IS0 | Q94IS0 avena strig |
| 45 | 33 | 66.0 | 765 | 10 | Q9SLP9 | Q9SLP9 luffa cylin |

ALIGNMENTS

RESULT 1
Q8T926 PRELIMINARY; PRT; 155 AA.
AC Q8T926;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DE Kazal-type proteinase inhibitor 1.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
ON NCBI_TaxID=5911;
RX [1]
RP SEQUENCE FROM N.A.
RA Turkewitz A.P., Haddad A.;
RT "A non-architectural cargo protein in Tetrahymena thermophila dense
RT core secretory granules."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075151; AAL79514.1; -;
DR InterPro; IPR002350; Kazal.
DR SMART; SM00280; KAZAL; 1.
SQ SEQUENCE 155 AA; 17608 MW; E438CC6E2110786B CRC64;

Query Match 86.0%; Score 43; DB 5; Length 155;
Best Local Similarity 70.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCXXIXXPVC 11
| | | | |
DB 31 GCPEIXPVC 40

RESULT 2
Q9VNL6 PRELIMINARY; PRT; 730 AA.
AC Q9VNL6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

```

DE CG1077 protein.
GN CG1077.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Poilard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RT Science 287:2183-2195(2000).
RL EMBL; AB003600; AAF51914.1; -.
DR FLYBase; FBgn0037405; CG1077.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002350; kazal.
DR Pfam; PF00050; kazal.
DR SMART; SM00280; KAZAL; 3.
RW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 730 AA; 80473 MW; 3390882D74E5A09 CRC64;

Query Match 76.0%; Score 38; DB 5; Length 730;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11
Db 150 CTRIYRVC 158

RESULT 3
Q29185 PRELIMINARY; PRT; 56 AA.
ID Q29185
AC Q29185;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

```

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamis I., Simpson M.C., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter S., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of *Drosophila melanogaster*,"
Science 287:2185-2195(2000).
[12]
SEQUENCE FROM N.A.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celiker S.,
Submitted (JUN-2002) to the ENBL/GenBank/DBJ databases.
EMBL: AF003680; AAF54297.1; -;
EMBL: AY118777; AAM50637.1; -;
FlyBase: FBgn0040532; CG8369.
SEQUENCE 94 AA, 10163 MW, 1A8EA3359E520788 CRC64;

Query Match 72.0%; Score 16; DB 5; Length 94;
Best Local Similarity 55.6%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps

QY 3 CXXIXYPCV 11
DB 37 CGEVYPCV 45

RESULT 6
Q9VE57 PRELIMINARY; PRT; 145 AA.
ID Q9VE57
AC Q9VE57
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG7695 protein.
GN CG7695
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]_TaxID=7227;
SEQUENCE FROM N.A.
STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Beeson X.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

| | | | | |
|-----------------------|--------|-----------------|---------------|------------|
| Query Match | 72.0%; | Score 36; | DB 5; | Length 94; |
| Best Local Similarity | 55.6%; | Pred. No. 5.2; | | |
| Matches | 5; | Conservative 1; | Mismatches 3; | Indels 0; |
| Matches | 5; | Conservative 1; | Mismatches 3; | Indels 0; |

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houstoun K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
DR EMBL; AE003723; AAF55572.1; --
DR FlyBase; FBgn0038631; CG7695.
DR GO; GO:004867; P:serine protease inhibitor activity; IEA.
DR InterPro; IPR002350; Kazal.
DR Pfam; PF00050; Kazal; 1.
DR SMART; SM00280; KAZAL; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 145 AA; 16581 MW; 4A52F2795CC67288 CRC64;

Query Match 72.0%; Score 36; DB 5; Length 145;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11
| | | | |
Db 95 CPDIYDPVC 103

RESULT 7
02037 PRELIMINARY; PRT; 1699 AA.
AC 02037;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Voltage-gated sodium channel homolog Bdnal.
GN BDNAL.
OS Bdnelloura candida.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Maricola; Bdellouridae; Bdellouridae; Bdelloura.
OX NCBI_TaxID=46766;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9744558; PubMed=930466;
RA Jezioriski M.C., Greenberg R.M., Anderson P.A.V.;
RT "Cloning of a putative voltage-gated sodium channel from the
RL turbellarian flatworm *Bdnelloura candida*.";
RT Parasitology 115:289-296 (1997).
DR EMBL; U93074; AAC63049.1; --
DR FIR; T31340; T31340.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.

DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M-channel_mlg.
DR InterPro; IPR001696; Na channel.
DR Pfam; PF00520; Ion trans; 4.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1699 AA; 197754 MW; F985D5F34D9CE62A CRC64;

Query Match 72.0%; Score 36; DB 5; Length 1699;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11
| | | | |
Db 469 CDDIYQPIC 477

RESULT 8
036986 PRELIMINARY; PRT; 140 AA.
AC 036986;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 18kDa unknown protein.
OS Lily symptomless virus (LSV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carliavirus.
OX NCBI_TaxID=12173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSV-Ko;
RA Ryu K.H., Ahn H.I., Kim S.J., Park W.M.;
RT "The nucleotide sequence of 3'-terminal region of lily symptomless
RT virus (LSV) Korean strain (LSV-Ko).";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015286; AAE70213.1; --
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002568; Carla_C4.
DR Pfam; PF01623; Carla_C4; 1.
SQ SEQUENCE 140 AA; 16113 MW; 5PA206989BDDA927 CRC64;

Query Match 70.0%; Score 35; DB 12; Length 140;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CXXIYXPVC 11
| | | | |
Db 86 CYRVFPVC 94

RESULT 9
083090 PRELIMINARY; PRT; 140 AA.
AC 083090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 16 kDa protein.
OS Lily symptomless virus (LSV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carliavirus.
OX NCBI_TaxID=12173;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.K., Kim Y.H., Lee S.Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43905; AAA95904.1; --
DR GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carlia_C4.
Pfam; PF01623; Carlia_C4; 1.
SEQUENCE 140 AA; 16051 MW; A190FA0BDE82AC39 CRC64;
ery Match 70.0%; Score 35; DB 12; Length 140;
st Local Similarity 55.6%; Pred. No. 12; Indels 0; Gaps 0;
atches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
3 CXXIYXPVC 11
86 CYRVYPPVC 94
1LT 10
16 PRELIMINARY; PRT; 222 AA.
Q95P16
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Thrombin inhibitor infestin (Fragment).
Triatoma infestans (Assassin bug).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
Panheteroptera; Cimicomorpha; Reduviidae; Triatominae; Triatoma.
NCBI_TaxID=30076;
SEQUENCE FROM N.A.
TISSUE=anterior midgut;
Campos I.T.N.; Amiro R.; Sampaio C.A.M.; Auerswald E.A.; Friedrich T.;
Lemaire H.-G.; Schenkman S.; Tanaka A.S.;
"Infestin, a novel thrombin inhibitor present in Triatoma infestans
midgut, a Chagas disease vector: cloning, expression and
characterization.";
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF360846; AK57342.1; --
HSP; P01001; IBSU.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
InterPro; IPR002350; kazal.
InterPro; IPR001239; Kazal_inhib.
Pfam; PF000050; kazal; 4.
PRINTS; PR00290; KAZALINHETR.
SMART; SM00280; KAZAL; 4.
PROSITE; PS00282; KAZAL; 4.
NON TER 1 1
CHAIN 1 >104 THROMBIN INHIBITOR INFESTIN.
NON TER 222 222
SEQUENCE 222 AA; 24370 MW; C9185168B4D41AC3 CRC64;
ery Match 70.0%; Score 35; DB 5; Length 222;
st Local Similarity 55.6%; Pred. No. 18;
atches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
3 CXXIYXPVC 11
117 CTRMYKPVC 125
ULT 11
659 PRELIMINARY; PRT; 385 AA.
Q92659 Q9ULB0;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Haptoglobin-related protein.
HPR OR A-259H10.2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97101114; PubMed=8945641;
Tabak S.; Lev A.; Valansi C.; Shalitin C.;
"transcriptionally active haptoglobin-related (Hpr) gene in Hepatoma
G2 and leukemia molt-4 cells.";
RL DNA Cell Biol. 15:1001-1007(1996).
RN [2]
RP SEQUENCE OF 40-385 FROM N.A.
RX MEDLINE=9425270; PubMed=10493829;
Lofthus B.J.; Kim U.J.; Sneddon V.P.; Kalush F.; Brandon R.;
Fuhmann J.; Mason T.; Crosby M.L.; Barnstead M.; Cronin L.;
Deslattes Mays A.; Cao Y.; Xu R.X.; Kang H.L.; Mitchell S.;
Richler E.E.; Harris P.C.; Venter J.C.; Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from
human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X89214; CAA61501.1; --
DR EMBL; AC004682; AAC27433.1; --
DR HSSP; P08709; 1FAK.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0002333; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR008292; Pept_S1_HapGnph.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PIRSF; PIRSF001137; Haptoglobin; 1.
DR Hydrolase; Protease; Serine protease.
FT VARIAT 376 376 H -> D.
KW SEQUENCE 385 AA; 43077 MW; 8445DD27A496188B CRC64;
Query Match 70.0%; Score 35; DB 4; Length 385;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 CXXIYXPVC 11
Db 8 CVCVYMPVC 16
RESULT 12
Q8F6E2 PRELIMINARY; PRT; 406 AA.
ID Q8F6E2
AC Q8F6E2; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LAL366.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011316; AAM4855.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 47362 MW; D088CDD194E7E93E CRC64;
Query Match 70.0%; Score 35; DB 16; Length 406;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GCXXIYXPVC 11
 || : ||
 Db 247 GCCELYIPSC 256

RESULT 13

ID Q9LKT8 PRELIMINARY; PRT; 724 AA.
 AC Q9LKT8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN T32B20.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA WashU;
 RT "The A. thaliana Genome Sequencing Project.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Wilson R.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF262041; AAF67366.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 724 AA; 83057 MW; D75EC74414C20317 CRC64;

Query Match 70.0%; Score 35; DB 10; Length 724;
 Best Local Similarity 40.0%; Pred. No. 54;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 GCXXIYXPVC 11
 || : ||
 Db 698 GCNAVHIFMC 707

RESULT 14.

ID Q91GK0 PRELIMINARY; PRT; 82 AA.
 AC Q91GK0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Epiphyas postvittana nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=70600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hyink O., Dellow R.A., Olsen M., Caradoc-Davies K.M.B., Drake K.,
 RA Ward V.K.;
 RT "The complete sequence of the Epiphyas postvittana
 nucleopolyhedrovirus genome.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY043265; AAK85615.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 82 AA; 9395 MW; 32D80D96EC0324AB CRC64;

Query Match 68.0%; Score 34; DB 12; Length 82;
 Best Local Similarity 44.4%; Pred. No. 12;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 CXXIYXPVC 11
 || : ||
 Db 74 CSALYVPLC 82

RESULT 15
 Q7TLU0
 ID Q7TLU0 PRELIMINARY; PRT; 82 AA.
 AC Q7TLU0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=208973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93033705; PubMed=1413988;
 RA Lee H.Y., Arif B., Dobos P., Krell P.;
 RT "Identification of bent DNA and ARS fragments in the genome of
 Choristoneura fumiferana nuclear polyhedrosis virus.";
 RL Virus Res. 24:249-264(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95297142; PubMed=7778276;
 RA Xie W.D., Arif B., Dobos P., Krell P.J.;
 RT "Identification and analysis of a putative origin of DNA replication
 in the Choristoneura fumiferana multinucleocapsid nuclear polyhedrosis
 virus genome.";
 RL Virology 209:409-419(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95297155; PubMed=7778286;
 RA Liu J.J., Carstens E.B.;
 RT "Identification, localization, transcription, and sequence analysis of
 the Choristoneura fumiferana nuclear polyhedrosis virus DNA polymerase
 gene.";
 RL Virology 209:538-549(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96030854; PubMed=7595348;
 RA Barrett J.W., Krell P.J., Arif B.M.;
 RT "Characterization, sequencing and phylogeny of the ecdysteroid UDP-
 glucosyltransferase gene from two distinct nuclear polyhedrosis
 viruses isolated from Choristoneura fumiferana.";
 RL J. Gen. Virol. 76:2447-2456(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96183379; PubMed=8610448;
 RA Qiu W., Liu J.J., Carstens E.B.;
 RT "Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
 expression in insect cells.";
 RL Virology 217:564-572(1996).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96400202; PubMed=8806578;
 RA Liu J.J., Carstens E.B.;
 RT "Identification, molecular cloning, and transcription analysis of the
 Choristoneura fumiferana nuclear polyhedrosis virus spindle-like
 protein gene.";
 RL Virology 223:396-400(1996).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20276145; PubMed=10814576;
 RA Lapointe R., Back D.W., Ding Q., Carstens E.B.;
 RT "Identification and molecular characterization of the Choristoneura
 fumiferana multicapsid nucleopolyhedrovirus genomic region encoding
 the regulatory genes pkip, p47, lef-12, and gta.";
 RL Virology 271:109-121(2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21854555; PubMed=11864738;
 RA Carstens E.B., Liu J.J., Dominy C.;
 RT "Identification and molecular characterization of the baculovirus

CFMPV early genes: ie-1, ie-2 and pe38. ";
Virus Res. 83:13-30(2002).

[9]

SEQUENCE FROM N.A.
de Jong J.G., Dominy C.N., Lauzon H.A., Arif B.M., Carstens E.B.,
Krell P.J.;

"Complete Genome of Choristoneura fumiferana Multiple
Nucleopolyhedrovirus."; to the EMBL/GenBank/DBJ databases.
Submitted (MAY-2002)

EMBL; AF512031; AAP29838.1; -.

Hypothetical protein.

SEQUENCE 82 AA; 9594 MW; BEBDEAD779830EF CRC64;

Very Match 68.0%; Score 34; DB 12; Length 82;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

3 CXXIYXPVC 11

| : | : |

74 CSALYPLC 82

Job completed: August 11, 2004, 13:09:25
Time : 36.0952 secs

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